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12AP1/E5 -- Viventia Biotech
 1964 -- Aventis
 20K growth hormone -- AMUR
 28P6/E6 -- Viventia Biotech
 3-Hydroxyphthaloyl-beta-lactoglobulin --
 4-IBB ligand gene therapy --
 64-Cu MAb conjugate TETA-1A3 --
 Mallinckrodt Institute of Radiology
 64-Cu MAb conjugate TETA-CT84.66
 64-Cu Trastuzumab TETA conjugate --
 Genentech
 A 200 -- Amgen
 A10255 -- Eli Lilly
 A1PDX -- Hedral Therapeutics
 A6 -- Angstrom
 aaAT-III -- Genzyme
 Abciximab -- Centocor
 ABI.001 -- Atlantic BioPharmaceuticals
 ABT-828 -- Abbott
 Accutin
 Actinohivin
 activin -- Biotech Australia, Human
 Therapeutics
 activin -- Curls
 AD 439 -- Tanox
 AD 519 -- Tanox
 Adalimumab -- Cambridge Antibody Tech.
 Adenocarcinoma vaccine -- Biomira -- NIS
 Adenosine A2B receptor antagonists --
 Adenosine Therapeutics
 ADP-001 -- Axis Genetics
 AF 13948 -- Affymax
 Afelimomab -- Knoll
 AFP-SCAN -- Immunomedics
 AG 2195 -- Corixa
 agalsidase alfa -- Transkaryotic Therapies
 agalsidase beta -- Genzyme
 AGENT -- Antisoma
 AI 300 -- Autolimmune
 AI-101 -- Teva
 AI-102 -- Teva
 AI-201 -- Autolimmune
 AI-301 -- Autolimmune
 AIDS vaccine -- ANRS, CIBG, Hesed
 Biomed, Hollis-Eden, Rome, United
 Biomedical, American Home Products,
 Maxygen
 airway receptor ligand -- IC Innovations
 AJvW 2 -- Ajinomoto
 AK 30 NGF -- Alkermes
 Albuferon -- Human Genome Sciences
 albumin -- Biogen, DSM Anti-Infectives,
 Genzyme Transgenics, PPL Therapeutics,
 TranXenoGen, Welfide Corp.
 aldesleukin -- Chiron
 alefacept -- Biogen
 Alemtuzumab --
 Allergy therapy -- ALK-Abello/Maxygen,
 ALK-Abello/RP Scherer
 allergy vaccines -- Allergy Therapeutics
 Alnidofibatide -- Aventis Pasteur
 Alnorine -- SRC VB VECTOR
 ALP 242 -- Gruenenthal
 Alpha antitrypsin -- Arriva/Hyland
 Immuno/ProMetic/Protease Sciences
 Alpha-1 antitrypsin -- Cutter, Bayer, PPL
 Therapeutics, Profile, ZymoGenetics,
 Arriva
 Alpha-1 protease inhibitor -- Genzyme
 Transgenics, Welfide Corp.
 Alpha-galactose fusion protein --
 Immunomedics
 Alpha-galactosidase A -- Research
 Corporation Technologies
 Alpha-glucosidase -- Genzyme, Novazyme
 Alpha-lactalbumin
 Alpha-L-iduronidase -- Transkaryotic
 Therapies, BioMarin
 alteplase -- Genentech
 alvircept sudotox -- NIH
 ALX1-11 -- sNPS Pharmaceuticals
 Alzheimer's disease gene therapy --

FIG. 1A

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AM-133 -- AMRAD
 Amb a 1 immunostim conj. -- Dynavax
 AMD 3100 -- AnorMED -- NIS
 AMD 3465 -- AnorMED -- NIS
 AMD 3465 -- AnorMED -- NIS
 AMD Fab -- Genentech
 Amediplase -- Menarini, Novartis
 AM-F9
 Amoebiasis vaccine
 Amphiregulin -- Octagene
 anakinra -- Amgen
 analgesic -- Nobex
 anacetim -- Amgen
 Anergix.RA -- Corixa, Organon
 Angiocidin -- InKine
 angiogenesis inhibitors -- ILEX
 AngioMab -- Antisoma
 Angiopoietins -- Regeneron/Procter & Gamble
 angiostatin -- EntreMed
 Angiostatin/endostatin gene therapy -- Genetix Pharmaceuticals
 angiotensin-II, topical -- Maret
 Anthrax -- EluSys Therapeutics/US Army Medical Research Institute
 Anthrax vaccine
 Anti platelet-derived growth factor D human monoclonal antibodies -- CuraGen
 Anti-17-1A/ MAb 3622W94 -- GlaxoSmithKline
 Anti-2C4 MAb -- Genentech
 anti-4-1BB monoclonal antibodies -- Bristol-Myers Squibb
 Anti-Adhesion Platform Tech. -- Cytovax
 Anti-adipocyte MAb -- Cambridge Antibody Tech./Obesity
 antiallergics -- Maxygen
 antiallergy vaccine -- Acambis
 Anti-alpha-4-integrin MAB
 Anti-angiogenesis monoclonal antibodies -- KS Biomedix/Schering AG
 Anti-B4 MAb-DC1 conjugate -- ImmunoGen
 Anti-B7 antibody PRIMATIZED -- IDEC
 Anti-B7-1 MAB 16-10A1
 Anti-B7-1 MAB 1G10
 Anti-B7-2 MAB GL-1
 Anti-B7-2-gelonin Immunotoxin -- Antibacterials/antifungals -- Diversa/IntraBiotics
 Anti-beta-amyloid monoclonal antibodies -- Cambridge Antibody Tech., Wyeth-Ayerst
 Anti-BLyS antibodies -- Cambridge Antibody Tech. /Human Genome Sciences
 Antibody-drug conjugates -- Seattle Genetics/Eos
 Anti-C5 MAB BB5-1 -- Alexion
 Anti-C5 MAB N19-8 -- Alexion
 Anti-C8 MAB anticancer cytokines -- BioPulse
 anticancer matrix -- Telios Integra
 Anticancer monoclonal antibodies -- ARIUS, Immunex
 anticancer peptides -- Maxygen, Micrologix
 anticancer prodrug Tech. -- Alexion Antibody Technologies
 anticancer Troy-Bodies -- Affite -- Affitech
 anticancer vaccine -- NIH
 anticancers -- Epimmune
 Anti-CCR5/CXCR4 sheep MAB -- KS Biomedix Holdings
 Anti-CD11a MAB KBA --
 Anti-CD11a MAB M17
 Anti-CD11a MAB TA-3 --
 Anti-CD11a MAB WT.1 --
 Anti-CD11b MAB -- Pharmacia
 Anti-CD11b MAB LM2
 Anti-CD154 MAB -- Biogen
 Anti-CD16-anti-CD30 MAB -- Biotest
 Anti-CD18 MAB -- Pharmacia
 Anti-CD19 MAB B43 --
 Anti-CD19 MAB -liposomal sodium butyrate conjugate --

FIG. 1B

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Anti-CD19 MAb-saporin conjugate --	Anti-CD4 MAb KT6
Anti-CD19-dsFv-PE38-immunotoxin --	Anti-CD4 MAb OX38
Anti-CD2 MAb 12-15 --	Anti-CD4 MAb PAP conjugate -- Bristol-Myers Squibb
Anti-CD2 MAb B-E2 -- Diaclone	Anti-CD4 MAb RIB 5-2
Anti-CD2 MAb OX34 --	Anti-CD4 MAb W3/25
Anti-CD2 MAb OX54 --	Anti-CD4 MAb YTA 3.1.2
Anti-CD2 MAb OX55 --	Anti-CD4 MAb YTS 177-9
Anti-CD2 MAb RM2-1	Anti-CD40 ligand MAb 5c8 -- Biogen
Anti-CD2 MAb RM2-2	Anti-CD40 MAb
Anti-CD2 MAb RM2-4	Anti-CD40 MAb 5D12 -- Tanox
Anti-CD20 MAb BCA B20	Anti-CD44 MAb A3D8
Anti-CD20-anti-Fc alpha RI bispecific MAb -- Medarex, Tenovus	Anti-CD44 MAb GKWA3
Anti-CD22 MAb-saporin-6 complex --	Anti-CD44 MAb IM7
Anti-CD3 immunotoxin --	Anti-CD44 MAb KM81
Anti-CD3 MAb 145-2C11 -- Pharming	Anti-CD44 variant monoclonal antibodies -- Corixa/Hebrew University
Anti-CD3 MAb CD4IgG conjugate -- Genentech	Anti-CD45 MAb BC8-I-131
Anti-CD3 MAb humanised -- Protein Design, RW Johnson	Anti-CD45RB MAb
Anti-CD3 MAb WT32	Anti-CD48 MAb HuLy-m3
Anti-CD3 MAb-ricin-chain-A conjugate --	Anti-CD48 MAb WM-63
Anti-CD3 MAb-xanthine-oxidase conjugate --	Anti-CD5 MAb -- Becton Dickinson
Anti-CD30 MAb BerH2 -- Medac	Anti-CD5 MAb OX19
Anti-CD30 MAb-saporin conjugate	Anti-CD6 MAb
Anti-CD30-scFv-ETA'-immunotoxin	Anti-CD7 MAb-PAP conjugate
Anti-CD38 MAb AT13/5	Anti-CD7 MAb-ricin-chain-A conjugate
Anti-CD38 MAb-saporin conjugate	Anti-CD8 MAb -- Amerimmune, Cytodyn, Becton Dickinson
Anti-CD3-anti-CD19 bispecific MAb	Anti-CD8 MAb 2-43
Anti-CD3-anti-EGFR MAb	Anti-CD8 MAb OX8
Anti-CD3-anti-interleukin-2-receptor MAb	Anti-CD80 MAb P16C10 -- IDEC
Anti-CD3-anti-MOV18 MAb -- Centocor	Anti-CD80 MAb P7C10 -- ID Vaccine
Anti-CD3-anti-SCLC bispecific MAb	Anti-CD8-idarubicin conjugate
Anti-CD4 idiotype vaccine	Anti-CEA MAb CE-25
Anti-CD4 MAb -- Centocor, IDEC Pharmaceuticals, Xenova Group	Anti-CEA MAb MN 14 -- Immunomedics
Anti-CD4 MAb 16H5	Anti-CEA MAb MN14-PE40 conjugate -- Immunomedics
Anti-CD4 MAb 4162W94 -- GlaxoSmithKline	Anti-CEA MAb T84.66-interleukin-2 conjugate
Anti-CD4 MAb B-F5 -- Diaclone	Anti-CEA sheep MAb -- KS Biomedix Holdings
Anti-CD4 MAb GK1-5	

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- Anti-cell surface monoclonal antibodies --
 Cambridge Antibody Tech. /Pharmacia
 Anti-c-erbB2-anti-CD3 bifunctional MAb --
 Otsuka
 Anti-CMV MAb -- Scotgen
 Anti-CTLA-4 MAb
 Anti-EGFR catalytic antibody -- Hesed
 Biomed
 anti-EGFR immunotoxin -- IVAX
 Anti-EGFR MAb -- Abgenix
 Anti-EGFR MAb 528
 Anti-EGFR MAb KSB 107 -- KS Biomedix
 Anti-EGFR MAb-DM1 conjugate --
 ImmunoGen
 Anti-EGFR MAb-LA1 --
 Anti-EGFR sheep MAb -- KS Biomedix
 Anti-FAP MAb F19-I-131
 Anti-Fas IgM MAb CH11
 Anti-Fas MAb Jo2
 Anti-Fas MAb RK-8
 Anti-Fit-1 monoclonal antibodies -- ImClone
 Anti-fungal peptides -- State University of
 New York
 antifungal tripeptides -- BTG
 Anti-ganglioside GD2 antibody-interleukin-2
 fusion protein -- Lexigen
 Anti-GM2 MAb -- Kyowa
 Anti-GM-CSF receptor monoclonal
 antibodies -- AMRAD
 Anti-gp130 MAb -- Tosoh
 Anti-HCA monoclonal antibodies --
 AltaRex/Epigen
 Anti-hCG antibodies -- Abgenix/AVI
 BioPharma
 Anti-heparanase human monoclonal
 antibodies -- Oxford
 Glycosciences/Medarex
 Anti-hepatitis C virus human monoclonal
 antibodies -- XTL Biopharmaceuticals
 Anti-HER-2 antibody gene therapy
 Anti-herpes antibody -- Epicyte
 Anti-HIV antibody -- Epicyte
 anti-HIV catalytic antibody -- Hesed Biomed
 anti-HIV fusion protein -- Idun
 anti-HIV proteins -- Cangene
 Anti-HM1-24 MAb -- Chugai
 Anti-hR3 MAb
 Anti-Human-Carcinoma-Antigen MAb --
 Epicyte
 Anti-ICAM-1 MAb -- Boehringer Ingelheim
 Anti-ICAM-1 MAb 1A-29 -- Pharmacia
 Anti-ICAM-1 MAb HA58
 Anti-ICAM-1 MAb YN1/1.7.4
 Anti-ICAM-3 MAb ICM3 -- ICOS
 Anti-idiotypic breast cancer vaccine 11D10
 Anti-idiotypic breast cancer vaccine
 ACA14C5 --
 Anti-idiotypic cancer vaccine -- ImClone
 Systems/Merck KGaA ImClone, Viventia
 Biotech
 Anti-idiotypic cancer vaccine 1A7 -- Titan
 Anti-idiotypic cancer vaccine 3H1 -- Titan
 Anti-idiotypic cancer vaccine TriAb -- Titan
 Anti-idiotypic Chlamydia trachomatis
 vaccine
 Anti-idiotypic colorectal cancer vaccine --
 Novartis
 Anti-idiotypic colorectal cancer vaccine --
 Onyvox
 Anti-idiotypic melanoma vaccine -- IDEC
 Pharmaceuticals
 Anti-idiotypic ovarian cancer vaccine ACA
 125
 Anti-idiotypic ovarian cancer vaccine AR54 -
 - AltaRex
 Anti-idiotypic ovarian cancer vaccine CA-
 125 -- AltaRex, Biomira
 Anti-IgE catalytic antibody -- Hesed Biomed
 Anti-IgE MAb E26 -- Genentech
 Anti-IGF-1 MAb
 anti-inflammatory -- GeneMax
 anti-inflammatory peptide -- BTG

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anti-integrin peptides -- Burnha	Anti-mu MAb -- Novartis
Anti-interferon-alpha-receptor MAb 64G12 -- Pharma Pacific Management	Anti-MUC-1 MAb
Anti-interferon-gamma MAb -- Protein Design Labs	Anti-Nogo-A MAb IN1
Anti-interferon-gamma polyclonal antibody -- - Dompe	Anti-nuclear autoantibodies -- Procyon
- Advanced Biotherapy	Anti-ovarian cancer monoclonal antibodies --
Anti-interleukin-10 MAb --	Anti-p185 monoclonal antibodies
Anti-interleukin-12 MAb --	Anti-p43 MAb
Anti-interleukin-1-beta polyclonal antibody -- R&D Systems	Antiparasitic vaccines
Anti-interleukin-2 receptor MAB 2A3	Anti-PDGF/bFGF sheep MAb -- KS Biomedix
Anti-interleukin-2 receptor MAB 33B3-1 -- Immunotech	Anti-properdin monoclonal antibodies -- Abgenix/Gliatech
Anti-interleukin-2 receptor MAB ART-18	Anti-PSMA MAB J591 -- BZL Biologics
Anti-interleukin-2 receptor MAB LO-Tact-1	Anti-Rev MAB gene therapy --
Anti-interleukin-2 receptor MAB Mikbeta1	Anti-RSV antibodies -- Epicyte, Intracell
Anti-interleukin-2 receptor MAB NDS61	Anti-RSV monoclonal antibodies -- Medarex/MedImmune, Applied Molecular Evolution/MedImmune
Anti-interleukin-4 MAB 11B11	Anti-RSV MAB, inhalation -- Alkermes/MedImmune
Anti-interleukin-5 MAB -- Wallace Laboratories	Anti-RT gene therapy
Anti-interleukin-6 MAB -- Centocor, Diacione, Pharmadigm	Antisense K-ras RNA gene therapy
Anti-interleukin-8 MAB -- Xenotech	Anti-SF-25 MAB
Anti-JL1 MAB	Anti-sperm antibody -- Epicyte
Anti-Klebsiella sheep MAB -- KS Biomedix Holdings	Anti-Tac(Fv)-PE38 conjugate
Anti-Laminin receptor MAB-liposomal doxorubicin conjugate	Anti-TAPA/CD81 MAB AMP1
Anti-LCG MAB -- Cytoclonal	Anti-tat gene therapy
Anti-lipopopolysaccharide MAB -- VitaResc	Anti-TCR-alpha-beta MAB H57-597
Anti-L-selectin monoclonal antibodies -- Protein Design Labs, Abgenix, Stanford University	Anti-TCR-alpha-beta MAB R73
Anti-MBL monoclonal antibodies -- Alexion/Brigham and Women's Hospital	Anti-tenascin MAB BC-4-l-131
Anti-MHC monoclonal antibodies	Anti-TGF-beta human monoclonal antibodies -- Cambridge Antibody Tech., Genzyme
Anti-MIF antibody humanised -- IDEC, Cytokine PharmaSciences	Anti-TGF-beta MAB 2G7 -- Genentech
Anti-MRSA/VRSA sheep MAB -- KS Biomedix Holdings	Anti-thrombin III -- Genzyme Transgenics, Aventis, Bayer, Behringwerke, CSL, Myriad
	Anti-Thy1 MAB
	Anti-Thy1.1 MAB

FIG. 1E

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Anti-tissue factor/factor VIIA sheep MAb -- KS Biomedix
 Anti-TNF monoclonal antibodies -- Centocor, Chiron, Peptech, Pharacia, Serono
 Anti-TNF sheep MAb -- KS Biomedix Holdings
 Anti-TNFalpha MAb -- Genzyme
 Anti-TNFalpha MAb B-C7 -- Diaclone
 Anti-tooth decay MAb -- Planet BioTech.
 antitumour RNases -- NIH
 Anti-VCAM MAb 2A2 -- Alexion
 Anti-VCAM MAb 3F4 -- Alexion
 Anti-VCAM-1 MAb
 Anti-VEC MAb -- ImClone
 Anti-VEGF MAb -- Genentech
 Anti-VEGF MAb 2C3
 Anti-VEGF sheep MAb -- KS Biomedix Holdings
 Anti-VLA-4 MAb HP1/2 -- Biogen
 Anti-VLA-4 MAb PS/2
 Anti-VLA-4 MAb R1-2
 Anti-VLA-4 MAb TA-2
 Anti-VRE sheep MAb -- KS Biomedix Holdings
 ANUP -- TranXenoGen
 ANUP-1 -- Pharis
 AOP-RANTES -- Senetek
 Apan-CH -- Praecis Pharmaceuticals
 APC-8024 -- Demegen
 ApoA-1 -- Milano, Pharmacia
 Apogen -- Alexion
 apolipoprotein A1 -- Avanir
 Apolipoprotein E -- Bio-Tech. General
 Applaggin -- Biogen
 aprotinin -- ProdiGene
 APT-070C -- AdProTech
 AR 177 -- Aronex Pharmaceuticals
 AR 209 -- Aronex Pharmaceuticals, Antigenics
 AR545C
 ARGENT gene delivery systems -- ARIAD
 Arresten
 ART-123 -- Asahi Kasei
 arylsulfatase B -- BioMarin
 Arylsulfatase B, Recombinant human -- BioMarin
 AS 1051 -- Ajinomoto
 ASI-BCL -- Intracell
 ATL-101 -- Alizyme
 atrial natriuretic peptide -- Pharis
 Aurintricarboxylic acid-high molecular weight
 autoimmune disorders -- GPC
 Biotech/MorphoSys
 Autoimmune disorders and transplant rejection -- Bristol-Myers Squibb/Genzyme
 Tra
 Autoimmune disorders/cancer -- Abgenix/Chiron, /CuraGen
 Autotaxin
 Avidin -- NeoRx
 axogenesis factor-1 -- Boston Life Sciences
 Axokine -- Regeneron
 B cell lymphoma vaccine -- Biomira
 B7-1 gene therapy -- BABS proteins -- Chiron
 BAM-002 -- Novelos Therapeutics
 Bay-16-9996 -- Bayer
 Bay-39-9437 -- Bayer
 Bay-50-4798 -- Bayer
 BB-10153 -- British Biotech
 BBT-001 -- Bolder BioTech.
 BBT-002 -- Bolder BioTech.
 BBT-003 -- Bolder BioTech.
 BBT-004 -- Bolder BioTech.
 BBT-005 -- Bolder BioTech.
 BBT-006 -- Bolder BioTech.
 BBT-007 -- Bolder BioTech.
 BCH-2763 -- Shire
 BCSF -- Millenium Biologix
 BDNF -- Regeneron -- Amgen

FIG. 1F

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Becaplermin -- Johnson & Johnson, Chiron
 Bectumomab -- Immunomedics
 Beta-adrenergic receptor gene therapy --
 University of Arkansas
 BI 51013 -- Behringwerke AG
 BIBH 1 -- Boehringer Ingelheim
 BIM-23190 -- Beaufour-Ipsen
 birch pollen immunotherapy -- Pharmacia
 bispecific fusion proteins -- NIH
 Bispecific Mab 2B1 -- Chiron
 Bitistatin
 BIWA 4 -- Boehringer Ingelheim
 blood substitute -- Northfield, Baxter Intl.
 BLP-25 -- Biomira
 BLS-0597 -- Boston Life Sciences
 BLYS -- Human Genome Sciences
 BLYS radiolabelled -- Human Genome
 Sciences
 BM 06021 -- Boehringer Mannheim
 BM-202 -- BioMarin
 BM-301 -- BioMarin
 BM-301 -- BioMarin
 BM-302 -- BioMarin
 BMP 2 -- Genetics Institute/Medtronic-
 Sofamor Danek, Genetics Institute/
 Collagenesis, Genetics
 Institute/Yamanouch
 BMP 2 gene therapy
 BMP 52 -- Aventis Pasteur, Biopharm
 BMP-2 -- Genetics Institute
 BMS 182248 -- Bristol-Myers Squibb
 BMS 202448 -- Bristol-Myers Squibb
 bone growth factors -- IsoTis
 BPC-15 -- Pfizer
 brain natriuretic peptide --
 Breast cancer -- Oxford
 GlycoSciences/Medarex
 Breast cancer vaccine -- Therion Biologics,
 Oregon
 BSSL -- PPL Therapeutics
 BST-2001 -- BioStratum
 BST-3002 -- BioStratum
 BTI 322 --
 butyrylcholinesterase -- Shire
 C 6822 -- COR Therapeutics
 C1 esterase inhibitor -- Pharming
 C3d adjuvant -- AdProTech
 CAB-2.1 -- Millennium
 calcitonin -- Inhale Therapeutics Systems,
 Aventis, Genetronics, TranXenoGen,
 Unigene, Rhone Poulenc Rohrer
 calcitonin -- oral -- Nobex, Emisphere,
 Pharmaceutical Discovery
 Calcitonin gene-related peptide -- Asahi
 Kasei -- Unigene
 calcitonin, human -- Suntory
 calcitonin, nasal -- Novartis, Unigene
 calcitonin, Panoderm -- Elan
 calcitonin, Peptitol -- Shire
 calcitonin, salmon -- Therapicon
 calin -- Biopharm
 Calphobindin I
 calphobindin I -- Kowa
 calreticulin -- NYU
 Campath-1G
 Campath-1M
 cancer therapy -- Cangene
 cancer vaccine -- Axlle, Aventis Pasteur,
 Center of Molecular Immunology, YM
 BioSciences, Cytos, Genzyme,
 Transgenics, GlobeImmune, Igeneon,
 ImClone, Virogenetics, InterCell, Iomai,
 Jenner Biotherapies, Memorial Sloan-
 Kettering Cancer Center, Sydney Kimmel
 Cancer Center, Novavax, Protein
 Sciences, Argonex, SIGA
 Cancer vaccine ALVAC-CEA B7.1 --
 Aventis Pasteur/Therion Biologics
 Cancer vaccine CEA-TRICOM -- Aventis
 Pasteur/Therion Biologics
 Cancer vaccine gene therapy -- Cantab
 Pharmaceuticals

FIG. 1G

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Cancer vaccine HER-2/neu -- Corixa	CETP vaccine -- Avant
Cancer vaccine THERATOPE -- Biomira	Cetorelix
cancer vaccine, PolyMASC -- Valentis	Cetuximab
Candida vaccine -- Corixa, Inhibitex	CGH 400 -- Novartis
Canstatin -- ILEX	CGP 42934 -- Novartis
CAP-18 -- Panorama	CGP 51901 -- Tanox
Cardiovascular gene therapy -- Collateral Therapeutics	CGRP -- Unigene
carperitide -- Suntory	CGS 27913 -- Novartis
Casocidin-1 -- Pharis	CGS 32359 -- Novartis
CAT 152 -- Cambridge Antibody Tech.	Chagas disease vaccine -- Corixa
CAT 192 -- Cambridge Antibody Tech.	chemokines -- Immune Response
CAT 213 -- Cambridge Antibody Tech.	CHH 380 -- Novartis
Catalase -- Enzo	chitinase -- Genzyme, ICOS
Cat-PAD -- Circassia	Chlamydia pneumoniae vaccine -- Antex Biologics
CB 0006 -- Celltech	Chlamydia trachomatis vaccine -- Antex Biologics
CCK(27-32) -- Akzo Nobel	Chlamydia vaccine -- GlaxoSmithKline
CCR2-641 -- NIH	Cholera vaccine CVD 103-HgR -- Swiss Serum and Vaccine Institute Berne
CD, Procept -- Paligent	Cholera vaccine CVD 112 -- Swiss Serum and Vaccine Institute Berne
CD154 gene therapy	Cholera vaccine inactivated oral -- SBL Vaccin
CD39 -- Immunex	Chrysalin -- Chrysalis BioTech.
CD39-L2 -- Hyseq	CI-782 -- Hitachi Kase
CD39-L4 -- Hyseq	Ciliary neurotrophic factor -- Fidia, Roche
CD4 fusion toxin -- Senetek	CIM project -- Active Biotech
CD4 IgG -- Genentech	CL 329753 -- Wyeth-Ayerst
CD4 receptor antagonists -- Pharmacopeia/Progenics	CL22, Cobra -- ML Laboratories
CD4 soluble -- Progenics	Clenoliximab -- IDEC
CD4, soluble -- Genzyme Transgenics	Clostridium difficile antibodies -- Epicyte
CD40 ligand -- Immunex	clotting factors -- Octagene
CD4-ricin chain A -- Genentech	CMB 401 -- Celltech
CD59 gene therapy -- Alexion	CNTF -- Sigma-Tau
CD8 TIL cell therapy -- Aventis Pasteur	Cocaine abuse vaccine -- Cantab, ImmuLogic, Scripps
CD8, soluble -- Avidex	coccidiomycosis vaccine -- Arizo
CD95 ligand -- Roche	collagen -- Type I -- Pharming
CDP 571 -- Celltech	Collagen formation inhibitors -- FibroGen
CDP 850 -- Celltech	
CDP 870 -- Celltech	
CDS-1 -- Ernest Orlando	
Cedelizumab -- Ortho-McNeil	
Cetermin -- Insmed	

FIG. 1H

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Collagen/hydroxyapatite/bone growth factor	CY 1747 -- Epimmune
-- Aventis Pasteur, Biopharm, Orquest	CY 1748 -- Epimmune
collagenase -- BioSpecifics	Cyanovirin-N
Colorectal cancer vaccine -- Wistar Institute	Cystic fibrosis therapy -- CBR/IVAX
Component B, Recombinant -- Serono	CYT 351
Connective tissue growth factor inhibitors --	cytokine Traps -- Regeneron
FibroGen/Taisho	cytokines -- Enzon, Cytoconal
Contortrostatin	Cytomegalovirus glycoprotein vaccine --
contraceptive vaccine -- Zonagen	Chiron, Aquila Biopharmaceuticals,
Contraceptive vaccine hCG	Aventis Pasteur, Virogenetics
Contraceptive vaccine male reversible --	Cytomegalovirus vaccine live -- Aventis
IMMUCON	Pasteur
Contraceptive vaccine zona pellucida --	Cytosine deaminase gene therapy --
Zonagen	GlaxoSmithKline
Copper-64 labelled MAb TETA-1A3 -- NCI	DA-3003 -- Dong-A
Coralyne	DAB389interleukin-6 -- Senetek
Corsevin M	DAB389interleukin-7
C-peptide analogues -- Schwarz	DAMP ^A -- Incyte Genomics
CPI-1500 -- Consensus	Daniplestim -- Pharmacia
CRF -- Neurobiological Tech.	darbepoetin alfa -- Amgen
cRGDFV pentapeptide --	DBI-3019 -- Diabetogen
CRL 1095 -- CytRx	DCC -- Genzyme
CRL 1336 -- CytRx	DDF -- Hyseq
CRL 1605 -- CytRx	decorin -- Integra, Telios
CS-560 -- Sankyo	defensins -- Large Scale Biology
CSF -- ZymoGenetics	DEGR-VIIa
CSF-G -- Hangzhou, Dong-A, Hanmi	Delimmunised antibody 3B6/22 AGEN
CSF-GM -- Cangene, Hunan, LG Chem	Deimmunised anti-cancer antibodies --
CSF-M -- Zarix	Biovation/Viragen
CT 1579 -- Merck Frosst	Dendroamide A
CT 1786 -- Merck Frosst	Dengue vaccine -- Bavarian Nordic, Merck
CT-112 ^A -- BTG	denileukin diftitox -- Ligand
CTB-134L -- Xenova	DES-1101 -- Desmos
CTC-111 -- Kaketsuken	desirudin -- Novartis
CTGF -- FibroGen	desmopressin -- Unigene
CTLA4-Ig -- Bristol-Myers Squibb	Desmoteplase -- Merck, Schering AG
CTLA4-Ig gene therapy --	Destabilase
CTP-37 -- AVI BioPharma	Diabetes gene therapy -- DeveloGen, Pfizer
C-type natriuretic peptide -- Suntory	Diabetes therapy -- Crucell
CVS 995 -- Corvas Int'l.	Diabetes type 1 vaccine -- Diamyd
CX 397 -- Nikko Kyodo	Therapeutics

FIG. 11

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DiaCIM -- YM BioSciences
 dialytic oligopeptides -- Research Corp
 Diamyd -- Diamyd Therapeutics
 DiaPep227 -- Pepgen
 DiavaX -- Corixa
 Diphtheria tetanus pertussis-hepatitis B vaccine -- GlaxoSmithKline
 DIR therapy -- Solis Therapeutics --
 DNase -- Genentech
 Dornase alfa -- Genentech
 Dornase alfa, inhalation -- Genentech
 Doxorubicin-anti-CEA MAb conjugate -- Immunomedics
 DP-107 -- Trimeris
 drotrecogin alfa -- Eli Lilly
 DTctGMCSF
 DTP-polio vaccine -- Aventis Pasteur
 DU 257-KM231 antibody conjugate -- Kyowa
 dural graft matrix -- Integra
 Duteplase -- Baxter Intl.
 DWP-401 -- Daewoong
 DWP-404 -- Daewoong
 DWP-408 -- Daewoong
 E coli O157 vaccine -- NIH
 E21-R -- BresaGen
 Eastern equine encephalitis virus vaccine --
 Echicetin --
 Echinhibin 1 --
 Echistatin -- Merck
 Echitamine --
 EC-SOD -- PPL Therapeutics
 EDF -- Ajinomoto
 EDN derivative -- NIH
 EDNA -- NIH
 Edobacomab -- XOMA
 Edrecolomab -- Centocor
 EF 5077
 Efalizumab -- Genentech
 EGF fusion toxin -- Seragen, Ligand
 EGF-P64k vaccine -- Center of Molecular Immunology
 EL 246 -- LigoCyte
 elastase inhibitor -- Synergen
 elcatonin -- Therapicon
 EMD 72000 -- Merck KGaA
 Emdogain -- BIORA
 emfillermin -- AMRAD
 Emoctakin -- Novartis
 enamel matrix protein -- BIORA
 Endo III -- NYU
 endostatin -- EntreMed, Pharis
 Enhancins -- Micrologix
 Enlimomab -- Isis Pharm.
 Enoxaparin sodium -- Pharmuka
 enzyme linked antibody nutrient depletion therapy -- KS Biomedix Holdings
 Eosinophil-derived neutralizing agent --
 EP-51216 -- Asta Medica
 EP-51389 -- Asta Medica
 EPH family ligands -- Regeneron
 Epidermal growth factor -- Hitachi Kasei, Johnson & Johnson
 Epidermal growth factor fusion toxin -- Senetek
 Epidermal growth factor-genistein --
 EPI-HNE-4 -- Dyax
 EPI-KAL2 -- Dyax
 Epoetin-alfa -- Amgen, Dragon Pharmaceuticals, Nanjing Huaxin
 Epratuzumab -- Immunomedics
 Epstein-Barr virus vaccine -- Aviron/SmithKline Beecham, Bioresearch
 Eptacog alfa -- Novo Nordisk
 Eptifibatide -- COR Therapeutics
 erb-38 --
 Erlizumab -- Genentech

FIG. 1J

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erythropoietin -- Alkermes, ProLease, Dong-Fas TR -- Human Genome Sciences
 A, Elanex, Genetics Institute, LG Chem,
 Protein Sciences, Serono, Snow Brand,
 SRC VB VECTOR, Transkaryotic
 Therapies
 Erythropoietin Beta -- Hoffman La Roche
 Erythropoietin/Epoetin alfa -- Chugai
 Escherichia coli vaccine -- North American
 Vaccine, SBL Vaccin, Swiss Serum and
 Vaccine Institute Berne
 etanercept -- Immunex
 examorelin -- Mediolanum
 exonuclease VII
 F 105 -- Centocor
 F-992 -- Fornix
 Factor IX -- Alpha Therapeutics, Welfide
 Corp., CSL, Genetics Institute/AHP,
 Pharmacia, PPL Therapeutics
 Factor IX gene therapy -- Cell Genesys
 Factor VII -- Novo Nordisk, Bayer, Baxter
 Intl.
 Factor VIIa -- PPL Therapeutics,
 ZymoGenetics
 Factor VIII -- Bayer Genentech, Beaufour-
 Ipsen, CLB, Inex, Octagen, Pharmacia,
 Pharming
 Factor VIII -- PEGylated -- Bayer
 Factor VIII fragments -- Pharmacia
 Factor VIII gene therapy -- Targeted
 Genetics
 Factor VIII sucrose formulation -- Bayer,
 Genentech
 Factor VIII-2 -- Bayer
 Factor VIII-3 -- Bayer
 Factor Xa inhibitors -- Merck, Novo Nordisk,
 Mochida
 Factor XIII -- ZymoGenetics
 Factors VIII and IX gene therapy -- Genetics
 Institute/Targeted Genetics
 Famoxin -- Genset
 Fas (delta) TM protein -- LXR BioTech.
 Felvizumab -- Scotgen
 FFR-VIIa -- Novo Nordisk
 FG-001 -- F-Gene
 FG-002 -- F-Gene
 FG-004 -- F-Gene
 FG-005 -- F-Gene
 FGF + fibrin -- Repair
 Fibrimage -- Bio-Tech. General
 fibrin-binding peptides -- ISIS Innovation
 fibrinogen -- PPL Therapeutics, Pharming
 fibroblast growth factor -- Chiron, NYU,
 Ramot, ZymoGenetics
 fibrolase conjugate -- Schering AG
 Filgrastim -- Amgen
 filgrastim -- PDA modified -- Xencor
 FLT-3 ligand -- Immunex
 FN18 CRM9 --
 follistatin -- Biotech Australia, Human
 Therapeutics
 follitropin alfa -- Alkermes, ProLease,
 PowderJect, Serono, Akzo Nobel
 Follitropin Beta -- Bayer, Organon
 FP 59
 FSH -- Ferring
 FSH + LH -- Ferring
 F-spondin -- CeNeS
 fusion protein delivery system -- UAB
 Research Foundation
 fusion toxins -- Boston Life Sciences
 G 5598 -- Genentech
 GA-II -- Transkaryotic Therapies
 Gamma-interferon analogues -- SRC VB
 VECTOR
 Ganirelix -- Roche
 gastric lipase -- Meristem
 Gavilimomab --
 G-CSF -- Amgen, SRC VB VECTOR
 GDF-1 -- CeNeS
 GDF-5 -- Biopharm
 GDNF -- Amgen

FIG. 1K

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gelsolin -- Biogen
 Gemtuzumab ozogamicin -- Celltech
 Gene-activated epoetin-alfa -- Aventis
 Pharma -- Transkaryotic Therapies
 Glanzmann thrombasthenia gene therapy --
 Glatiramer acetate -- Yeda
 glial growth factor 2 -- CeNeS
 GLP-1 -- Amylin, Suntory, TheraTech,
 Watson
 GLP-1 peptide analogues -- Zealand
 Pharmaceuticals
 glucagon -- Eli Lilly, ZymoGenetics
 Glucagon-like peptide-1 7-36 amide --
 Suntory
 Glucocerebrosidase -- Genzyme
 glutamate decarboxylase -- Genzyme
 Transgenics
 Glycoprotein S3 -- Kureha
 GM-CSF -- Immunex
 GM-CSF tumour vaccine -- PowderJect
 GnRH immunotherapeutic -- Protherics
 gp75 antigen -- ImClone
 gp96 -- Antigenics
 GPI 0100 -- Galenica
 GR 4991W93 -- GlaxoSmithKline
 Granulocyte colony-stimulating factor --
 Dong-A
 Granulocyte colony-stimulating factor
 conjugate
 grass allergy therapy -- Dynavax
 GRF1-44 -- ICN
 Growth Factor -- Chiron, Atrigel, Atrix,
 Innogenetics, ZymoGenetics, Novo
 growth factor peptides -- Biotherapeutics
 growth hormone -- LG Chem
 growth hormone, Recombinant human --
 SeroNo
 GT 4086 -- Gliatech
 GW 353430 -- GlaxoSmithKline
 GW-278884 -- GlaxoSmithKline
 H 11 -- Viventia Biotech
 H5N1 influenza A virus vaccine -- Protein
 Sciences
 haemoglobin -- Biopure
 haemoglobin 3011, Recombinant -- Baxter
 Healthcare
 haemoglobin crosfumaril -- Baxter Intl.
 haemoglobin stabilized -- Ajinomoto
 haemoglobin, recombinant -- Apex
 HAF -- Immune Response
 Hantavirus vaccine
 HB 19
 HBNF -- Regeneron
 HCC-1 -- Pharis
 hCG -- Milkhaus
 hCG vaccine -- Zonagen
 HE-317 -- Hollis-Eden Pharmaceuticals
 Heat shock protein cancer and influenza
 vaccines -- StressGen
 Helicobacter pylori vaccine -- Acambis,
 AstraZeneca/CSL, Chiron, Provalis
 Helistat-G -- GalaGen
 Hemolink -- Hemosol
 hepapoietin -- Snow Brand
 heparanase -- InSight
 heparinase I -- Ibex
 heparinase III -- Ibex
 Hepatitis A vaccine -- American Biogenetic
 Sciences
 Hepatitis A vaccine inactivated
 Hepatitis A vaccine Nothav -- Chiron
 Hepatitis A-hepatitis B vaccine --
 GlaxoSmithKline
 hepatitis B therapy -- Tripep
 Hepatitis B vaccine -- Amgen, Chiron SpA,
 Meiji Milk, NIS, Prodeva, PowderJect,
 Rhein Biotech
 Hepatitis B vaccine recombinant -- Evans
 Vaccines, Epitex Combiotech, Genentech,
 MedImmune, Merck Sharp & Dohme,
 Rhein Biotech, Shantha Biotechnics,
 Vector, Yeda

FIG. 1L

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- Hepatitis B vaccine recombinant TGP 943 -- HIV peptides -- American Home Products
Takeda
HIV vaccine -- Applied bioTech., Axis
Genetics, Biogen, Bristol-Myers Squibb,
Genentech, Korea Green Cross, NIS,
Hepatitis C vaccine -- Bavarian Nordic, Oncogen, Protein Sciences Corporation,
Chiron, Innogenetics Acambis, Terumo, Tonen Corporation, Wyeth-
Hepatitis D vaccine -- Chiron Vaccines Ayerst, Wyeth-Lederle Vaccines-Malvern,
Hepatitis E vaccine recombinant -- Genelabs/GlaxoSmithKline, Novavax Advanced BioScience Laboratories,
hepatocyte growth factor -- Panorama, Bavarian Nordic, Bavarian Nordic/Statens
Sosei
hepatocyte growth factor kringle fragments - Serum Institute, GeneCure, Immune
- EntrelMed Response, Progenics, Theron Biologics,
United Biomedical, Chiron
Her-2/Neu peptides -- Corixa
HIV vaccine vCP1433 -- Aventis Pasteur
Herpes simplex glycoprotein DNA vaccine -- Merck, Wyeth-Lederle Vaccines-Malvern, HIV vaccine vCP1452 -- Aventis Pasteur
Genentech, GlaxoSmithKline, Chiron, HIV vaccine vCP205 -- Aventis Pasteur
Takeda HL-9 -- American BioScience
Herpes simplex vaccine -- Cantab HM-9239 -- Cytran
Pharmaceuticals, CEL-SCI, Henderson HML-103 -- Hemosol
Morley HML-104 -- Hemosol
HML-105 -- Hemosol
Herpes simplex vaccine live -- ImClone HML-109 -- Hemosol
Systems/Wyeth-Lederle, Aventis Pasteur HML-110 -- Hemosol
HGF derivatives -- Dompe HML-121 -- Hemosol
hiAPP vaccine -- Crucell hNLP -- Pharis
Hib-hepatitis B vaccine -- Aventis Pasteur Hookworm vaccine
HIC 1 host-vector vaccines -- Henogen
HIP-- Altachem HPM 1 -- Chugai
Hirudins -- Biopharma, Cangene, Dongkook, HPV vaccine -- MediGene
Japan Energy Corporation, Pharmacia Corporation, SIR International, Sanofi-
Synthelabo, Sotragene, Rhein Biotech HSA -- Meristem
HIV edible vaccine -- ProdiGene HSF -- StressGen
HIV gp120 vaccine -- Chiron, Ajinomoto, HSP carriers -- Weizmann, Yeda, Peptor
GlaxoSmithKline, ID Vaccine, Progenics, HSPPC-70 -- Antigenics
VaxGen HSPPC-96 -- pathogen-derived --
Antigenics
HIV gp120 vaccine gene therapy -- HSV 863 -- Novartis
HIV gp160 DNA vaccine -- PowderJect, HTLV-I DNA vaccine
Aventis Pasteur, Oncogen, Hyland HTLV-I vaccine
Immuno, Protein Sciences HTLV-II vaccine -- Access
HIV gp41 vaccine -- Panacos HU 901 -- Tanox
HIV HGP-30W vaccine -- CEL-SCI Hu23F2G -- ICOS
HIV immune globulin -- Abbott, Chiron HuHMF61

FIG. 1M

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HumaLYM -- Intracell	HuMax-IL15 -- Genmab
Human krebs statika -- Yamanouchi	HYB 190 -- Hybridon
human monoclonal antibodies --	HYB 676 -- Hybridon
Abgenix/Biogen, Abgenix/ Corixa,	I-125 Mab A33 -- Celltech
Abgenix/ImmuneX, Abgenix/Lexicon,	Ibritumomab tiuxetan -- IDEC
Abgenix/ Pfizer, Athersys/Medarex,	IBT-9401 -- Ibex
Biogen/MorphoSys, CAT/Searle,	IBT-9402 -- Ibex
Centocor/Medarex, Corixa/Kirin Brewery,	IC 14 -- ICOS
Corixa/Medarex, Eos BioTech./Medarex,	Idarubicin anti-Ly-2.1 --
Eos/Xenerex, Exelixis/Protein Design	IDEC 114 -- IDEC
Labs, ImmunoGen/ Raven,	IDEC 131 -- IDEC
Medarex/B.Twelve,	IDEC 152 -- IDEC
MorphoSys/ImmunoGen, XTL	IDM 1 -- IDM
Biopharmaceuticals/Dyax,	IDPS -- Hollis-Eden Pharmaceuticals
Human monoclonal antibodies --	iduronate-2-sulfatase -- Transkaryotic
Medarex/Northwest Biotherapeutics,	Therapies
Medarex/Seattle Genetics	IGF/IBP-2-13 -- Pharis
human netrin-1 -- Exelixis	IGN-101 -- Igeneon
human papillomavirus antibodies -- Epicyte	IK HIR02 -- Iketon
Human papillomavirus vaccine -- Biotech	IL-11 -- Genetics Institute/AHP
Australia, IDEC, StressGen	IL-13-PE38 -- NeoPharm
Human papillomavirus vaccine MEDI 501 --	IL-17 receptor -- ImmuneX
MedImmune/GlaxoSmithKline	IL-18BP -- Yeda
Human papillomavirus vaccine MEDI	IL-1Hy1 -- Hyseq
503/MEDI 504 --	IL-1B -- Celltech
MedImmune/GlaxoSmithKline	IL-1B adjuvant -- Celltech
Human papillomavirus vaccine TA-CIN --	IL-2 -- Chiron
Cantab Pharmaceuticals	IL-2 + IL-12 -- Hoffman La-Roche
Human papillomavirus vaccine TA-HPV --	IL-6/sIL-6R fusion -- Hadasit
Cantab Pharmaceuticals	IL-6R derivative -- Tosoh
Human papillomavirus vaccine TH-GW --	IL-7-Dap 389 fusion toxin -- Ligand
Cantab/GlaxoSmithKline	IM-862 -- Cytran
human polyclonal antibodies -- Biosite/Eos	IMC-1C11 -- ImClone
BioTech./ Medarex	imiglucerase -- Genzyme
human type II anti factor VIII monoclonal	Immune globulin intravenous (human) --
antibodies -- ThromboGenics	Hoffman La Roche
humanised anti glycoprotein Ib murine	immune privilege factor -- Proneuron
monoclonal antibodies -- ThromboGenics	Immunocal -- Immunotec
HumaRAD -- Intracell	Immunogene therapy -- Briana Bio-Tech
HuMax EGFR -- Genmab	Immunoliposomal 5-fluorodeoxyuridine-
HuMax-CD4 -- Medarex	dipalmitate --

FIG. 1N

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immunosuppressant vaccine -- Axlle
 immunotoxin -- Antisoma, NIH
 ImmuRAIT-Re-188 -- Immunomedics
 imreg-1 -- Imreg
 infertility -- Johnson & Johnson, E-TRANS
 Influenza virus vaccine -- Aventis Pasteur,
 Protein Sciences
 inhibin -- Biotech Australia, Human
 Therapeutics
 Inhibitory G protein gene therapy
 INKP-2001 -- InKine
 Inolimomab -- Diaclone
 insulin -- AutoImmune, Altea, Biobras,
 BioSante, Bio-Tech. General, Chong Kun
 Dang, Emisphere, Flamel, Provalis, Rhein
 Biotech, TranXenoGen
 insulin (bovine) -- Novartis
 insulin analogue -- Eli Lilly
 Insulin Aspart -- Novo Nordisk
 insulin detemir -- Novo Nordisk
 insulin glargine -- Aventis
 insulin inhaled -- Inhale Therapeutics
 Systems, Alkermes
 insulin oral -- Inovax
 insulin, AeroDose -- AeroGen
 insulin, AERx -- Aradigm
 insulin, BEODAS -- Elan
 insulin, Biphax -- Helix
 insulin, buccal -- Generex
 insulin, i2R -- Flemington
 insulin, intranasal -- Bentley
 insulin, oral -- Nobex, Unigene
 insulin, Orasome -- Endorex
 insulin, ProMaxx -- Epic
 insulin, Quadrant -- Elan
 insulin, recombinant -- Aventis
 insulin, Spiros -- Elan
 insulin, Transfersome -- IDEA
 insulin, Zymo, recombinant -- Novo Nordisk
 insulinotropin -- Scios
 Insulysin gene therapy --
 integrin antagonists -- Merck
 Interferon (Alpha2) -- SRC VB VECTOR,
 Viragen, Dong-A, Hoffman La-Roche,
 Genentech
 Interferon -- BioMedicines, Human Genome
 Sciences
 Interferon (Alfa-n3) -- Interferon Sciences
 Intl.
 Interferon (Alpha), Biphax -- Helix
 Interferon (Alpha) -- Amgen, BioNative,
 Novartis, Genzyme Transgenics,
 Hayashibara, Inhale Therapeutics
 Systems, Medusa, Flamel, Dong-A,
 GeneTrol, Nastech, Shantha,
 Wassermann, LG Chem, Sumitomo,
 Aventis, Behring EGIS, Pepgen, Servier,
 Rhein Biotech,
 Interferon (Alpha2A)
 Interferon (Alpha2B) -- Enzon, Schering-
 Plough, Biogen, IDEA
 Interferon (Alpha-N1) -- GlaxoSmithKline
 Interferon (beta) -- Rentschler, GeneTrol,
 Meristem, Rhein Biotech, Toray, Yeda,
 Daiichi, Mochida
 Interferon (Beta1A) -- Serono, Biogen
 Interferon (beta1A), Inhale -- Biogen
 Interferon (B1b) -- Chiron
 Interferon (tau) -- Pepgen
 Interferon alfacon-1 -- Amgen
 Interferon alpha-2a vaccine
 Interferon Beta 1b -- Schering/Chiron,
 InterMune
 Interferon Gamma -- Boehringer Ingelheim,
 Sheffield, Rentschler, Hayashibara
 Interferon receptor, Type I -- Serono
 Interferon (Gamma1B) -- Genentech
 Interferon-alpha-2b + ribavirin -- Biogen,
 ICN
 Interferon-alpha-2b gene therapy --
 Schering-Plough
 Interferon-con1 gene therapy --

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interleukin-1 antagonists -- Dompe
 Interleukin-1 receptor antagonist -- Abbott
 Bloersearch, Pharmacia
 Interleukin-1 receptor type I -- Immunex
 interleukin-1 receptor Type II -- Immunex
 Interleukin-10 -- DNAX, Schering-Plough
 Interleukin-10 gene therapy --
 interleukin-12 -- Genetics Institute, Hoffman
 La-Roche
 interleukin-13 -- Sanofi
 Interleukin-13 antagonists -- AMRAD
 Interleukin-13-PE38QQR
 interleukin-15 -- Immunex
 interleukin-16 -- Research Corp
 interleukin-18 -- GlaxoSmithKline
 Interleukin-1-alpha -- Immunex/Roche
 interleukin-2 -- SRC VB VECTOR,
 Ajinomoto, Biomira
 Interleukin-3 -- Cangene
 Interleukin-4 -- Immunology Ventures,
 Sanofi Winthrop, Schering-Plough,
 Immunex/ Sanofi Winthrop, Bayer, Ono
 Interleukin-4 + TNF-Alpha -- NIH
 interleukin-4 agonist -- Bayer
 interleukin-4 fusion toxin -- Ligand
 Interleukin-4 receptor -- Immunex, Immun
 Interleukin-6 -- Ajinomoto, Cangene, Yeda,
 Genetics Institute, Novartis
 interleukin-6 fusion protein --
 interleukin-6 fusion toxin -- Ligand, Sero
 Interleukin-7 -- IC Innovations
 interleukin-7 receptor -- Immunex
 interleukin-8 antagonists -- Kyowa
 Hakko/Millennium/Pfizer
 interleukin-9 antagonists -- Genaera
 interleukins -- Cel-Sci
 Iodine I 131 tositumomab -- Corixa
 Ior EPOCIM -- Center of Molecular
 Immunology
 Ior-P3 -- Center of Molecular Immunology
 IP-10 -- NIH
 IPF -- Metabolex
 IR-501 -- Immune Response
 ISIS 9125 -- Isis Pharmaceuticals
 ISURF No. 1554 -- Millennium
 ISURF No. 1866 -- Iowa State Univer.
 ITF-1697 -- Italfarmaco
 IxC 162 -- Ixion
 J 695 -- Cambridge Antibody Tech.,
 Genetics Inst., Knoll
 Jagged + FGF -- Repair
 JKC-362 -- Phoenix Pharmaceuticals
 JTP-2942 -- Japan Tobacco
 Juman monoclonal antibodies --
 Medarex/Raven
 K02 -- Axs Pharmaceuticals
 Keliximab -- IDEC
 Keyhole limpet haemocyanin
 KGF -- Amgen
 KM 871 -- Kyowa
 KPI 135 -- Scios
 KPI-022 -- Scios
 Kringle 5
 KSB 304
 KSB-201 -- KS Biomedix
 L 696418 -- Merck
 L 703801 -- Merck
 L1 -- Acorda
 L-761191 -- Merck
 lactoferrin -- Meristem, Pharming, Agennix
 lactoferrin cardio -- Pharming
 LAG-3 -- Sero
 LAIT -- GEMMA
 LAK cell cytotoxin -- Arizona
 lamellarins -- PharmaMar/University of
 Malaga
 laminin A peptides -- NIH
 lanoteplase -- Genetics Institute
 Iaronidase -- BioMarin
 Lassa fever vaccine
 LCAT -- NIH
 LDP 01 -- Millennium

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LDP 02 -- Millennium
 Lecithinized superoxide dismutase --
 Seikagaku
 LeIF adjuvant -- Corixa
 leishmaniasis vaccine -- Corixa
 lenercept -- Hoffman La-Roche
 Lenograstim -- Aventis, Chugai
 lepirudin -- Aventis
 leptin -- Amgen, IC Innovations
 Leptin gene therapy -- Chiron Corporation
 leptin, 2nd-generation -- Amgen
 leridistim -- Pharmacia
 leuprolide, ProMaxx -- Epic
 leuprorelin, oral -- Unigene
 LeuTech -- Papatin
 LEX 032 -- SuperGen
 LiDEPT -- Novartis
 lipase -- Altus Biologics
 lipid A vaccine -- EntreMed
 lipid-linked anchor Tech. -- ICRT, ID
 Biomedical
 liposome-CD4 Tech. -- Sheffield
 Listeria monocytogenes vaccine
 LMB 1
 LMB 7
 LMB 9 -- Battelle Memorial Institute, NIH
 LM-CD45 -- Cantab Pharmaceuticals
 lovastatin -- Merck
 LSA-3
 LT- β receptor -- Biogen
 lung cancer vaccine -- Corixa
 lusupultide -- Scios
 L-Vax -- AVAX
 LY 355455 -- Eli Lilly
 LY 366405 -- Eli Lilly
 LY-355101 -- Eli Lilly
 Lyme disease DNA vaccine -- Vical/Aventis
 Pasteur
 Lyme disease vaccine -- Aquila
 Biopharmaceuticals, Aventis, Pasteur,
 Symbicom, GlaxoSmithKline, Hyland
 Immuno, MedImmune
 Lymphocytic choriomeningitis virus vaccine
 lymphoma vaccine -- Biomira, Genitope
 LYP18
 lys plasminogen, recombinant
 Lysosomal storage disease gene therapy --
 Avigen
 lysostaphin -- Nutrition 21
 M 23 -- Gruenenthal
 M1 monoclonal antibodies -- Acorda
 Therapeutics
 MA 16N7C2 -- Corvas Intl.
 malaria vaccine -- GlaxoSmithKline,
 AdProTech, Antigenics, Apovia, Aventis
 Pasteur, Axis Genetics, Behringwerke,
 CDCP, Chiron Vaccines, Genzyme
 Transgenics, Hawaii, MedImmune, NIH,
 NYU, Oxon, Roche/Saramane, Biotech
 Australia, Rx Tech
 Malaria vaccine CDC/NIIMALVAC-1
 malaria vaccine, multicomponent
 mammaglobin -- Corixa
 mammastatin -- Biotherapeutics
 mannan-binding lectin -- Natlmmu
 mannan-MUC1 -- Psiron
 MAP 30
 Marinovir -- Phytera
 MARstem -- Maret
 MB-015 -- Mochida
 MBP -- ImmuLogic
 MCI-028 -- Mitsubishi-Tokyo
 MCF -- Human Genome Sciences
 MDC -- Advanced BioScience -- Akzo
 Nobel, ICOS
 MDX 11 -- Medarex
 MDX 210 -- Medarex
 MDX 22 -- Medarex
 MDX 22

FIG. 1Q

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MDX 240 -- Medarex	Methionine lyase gene therapy --
MDX 33	AntiCancer
MDX 44 -- Medarex	Met-RANTES -- Genexa Biomedical,
MDX 447 -- Medarex	Serono
MDX H210 -- Medarex	Metreleptin
MDX RA -- Houston BioTech., Medarex	MGDF -- Kirin
ME-104 -- Pharmexa	MGV -- Progenics
Measles vaccine	micrin -- Endocrine
Mecasmerin -- Cephalon/Chiron, Chiron	microplasmin -- ThromboGenics
MEDI 488 -- MedImmune	MIF -- Genetics Institute
MEDI 500	migration inhibitory factor -- NIH
MEDI 507 -- BioTransplant	Mim CD4.1 -- Xyte Therapies
melanin concentrating hormone --	mirostipen -- Human Genome Sciences
Neurocrine Biosciences	MK 852 -- Merck
melanocortins -- OMRF	Mobenakin -- NIS
Melanoma monoclonal antibodies -- Viragen	molgramostim -- Genetics Institute, Novartis
melanoma vaccine -- GlaxoSmithKline,	monoclonal antibodies -- Abgenix/Celltech,
Akzo Nobel, Avant, Aventis Pasteur,	Immusol/ Medarex, Viragen/ Roslin
Bavarian Nordic, Biovector, CancerVax,	Institute, Cambridge Antibody Tech./Elan
Genzyme Molecular Oncology, Humbolt,	MAb 108 --
ImClone Systems, Memorial, NYU, Oxxon	MAb 10D5 --
Melanoma vaccine Magevac -- Therion	MAb 14.18-interleukin-2 immunocytokine --
memory enhancers -- Scios	Lexigen
meningococcal B vaccine -- Chiron	MAb 14G2a --
meningococcal vaccine -- CAMR	MAb 15A10 --
Meningococcal vaccine group B conjugate -	MAb 170 -- Biomira
- North American Vaccine	MAb 177Lu CC49 --
Meningococcal vaccine group B	MAb 17F9
recombinant -- BioChem Vaccines,	MAb 1D7
Microscience	MAb 1F7 -- Immune Network
Meningococcal vaccine group Y conjugate -	MAb 1H10-doxorubicin conjugate
- North American Vaccine	MAb 26-2F
Meningococcal vaccine groups A B and C	MAb 2A11
conjugate -- North American Vaccine	MAb 2E1 -- RW Johnson
Mepolizumab -- GlaxoSmithKline	MAb 2F5
Metastatin -- EntreMed, Takeda	MAb 31.1 -- International BiImmune
Met-CkB7 -- Human Genome Sciences	Systems
met-enkephalin -- TNI	MAb 32 -- Cambridge Antibody Tech.,
METH-1 -- Human Genome Sciences	Peptech
methioninase -- AntiCancer	MAb 323A3 -- Centocor
	MAb 3C5

FIG. 1R

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MAb 3F12	MAb C242-PE conjugate
MAb 3F8	MAb c30-6
MAb 42/6	MAb CA208-cytorhodin-S conjugate --
MAb 425 -- Merck KGaA	Hoechst Japan
MAb 447-52D -- Merck Sharp & Dohme	MAb CC49 -- Enzon
MAb 45-2D9- -- haematoporphyrin	MAb ch14.18 --
conjugate	MAb CH14.18-GM-CSF fusion protein --
MAb 4B4	Lexigen
MAb 4E3-CPA conjugate -- BCM Oncologia	MAb chCE7
MAb 4E3-daunorubicin conjugate	MAb CI-137 -- AMRAD
MAb 50-6	MAb cisplatin conjugate
MAb 50-61A -- Institut Pasteur	MAb CLB-CD19
MAb 5A8 -- Biogen	MAb CLB-CD19v
MAb 791T/36-methotrexate conjugate	MAb CLL-1 -- Peregrine
MAb 7c11.e8	MAb CLL-1-GM-CSF conjugate
MAb 7E11 C5-selenocystamine conjugate	MAb CLL-1-IL-2 conjugate -- Peregrine
MAb 93KA9 -- Novartis	MAb CLN IgG -- doxorubicin conjugates
MAb A5B7-cisplatin conjugate --	MAb conjugates -- Tanox
Biodynamics Research, Pharmacia	MAb D612
MAb A5B7-I-131	MAb Dal B02
MAb A7	MAb DC101 -- ImClone
MAb A717 -- Exocell	MAb EA 1 --
MAb A7-zinostatin conjugate	MAb EC708 -- Biovation
MAb ABX-RB2 -- Abgenix	MAb EP-5C7 -- Protein Design Labs
MAb ACA 11	MAb ERIC-1 -- ICRT
MAb AFP-I-131 -- Immunomedics	MAb F105 gene therapy
MAb AP1	MAb FC 2.15
MAb AZ1	MAb G250 -- Centocor
MAb B3-LysPE40 conjugate	MAb GA6
MAb B4 -- United Biomedical	MAb GA733
MAb B43 Genistein-conjugate	MAb Gliomab-H -- Viventia Biotech
MAb B43.13-Tc-99m -- Biomira	MAb HB2-saporin conjugate
MAb B43-PAP conjugate	MAb HD 37 --
MAb B4G7-gelonin conjugate	MAb HD37-ricin chain-A conjugate
MAb BCM 43-daunorubicin conjugate --	MAb HNK20 -- Acambis
BCM Oncologia	MAb huN901-DM1 conjugate --
MAb BIS-1	ImmunoGen
MAb BMS 181170 -- Bristol-Myers Squibb	MAb I-131 CC49 -- Corixa
MAb BR55-2	MAb ICO25
MAb BW494	MAb ICR12-CPG2 conjugate
MAb C 242-DM1 conjugate -- ImmunoGen	MAb ICR-62

FIG. 1S

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MAb IRac-ricin A conjugate	MAb R-24
MAb K1	MAb R-24 α Human GD3 -- Celltech
MAb KS1-4-methotrexate conjugate	MAb RFB4-ricin chain A conjugate
MAb L6 -- Bristol-Myers Squibb, Oncogen	MAb RFT5-ricin chain A conjugate
MAb LICO 16-88	MAb SC 1
MAb LL2-I-131 -- Immunomedics	MAb SM-3 -- ICRT
MAb LL2-Y90	MAb SMART 1D10 -- Protein Design Labs
MAb LS2D617 -- Hybritech	MAb SMART ABL 364 -- Novartis
MAb LYM-1-gelonin conjugate	MAb SN6f
MAb LYM-1-I-131	MAb SN6f-deglycosylated ricin A chain
MAb LYM-1-Y-90	conjugate --
MAb LYM-2 -- Peregrine	MAb SN6j
MAb M195	MAb SN7-ricin chain A conjugate
MAb M195-bismuth 213 conjugate --	MAb T101-Y-90 conjugate -- Hybritech
Protein Design Labs	MAb T-88 -- Chiron
MAb M195-gelonin conjugate	MAb TB94 -- Cancer ImmunoBiology
MAb M195-I-131	MAb TEC 11
MAb M195-Y-90	MAb TES-23 -- Chugai
MAb MA 33H1 -- Sanofi	MAb TM31 -- Avant
MAb MAD11	MAb TNT-1 -- Cambridge Antibody Tech.,
MAb Mgb2	Peregrine
MAb MINT5	MAb TNT-3
MAb MK2-23	MAb TNT-3 -- IL2 fusion protein --
MAb MOC31 ETA(252-613) conjugate	MAb TP3-At-211
MAb MOC-31-In-111	MAb TP3-PAP conjugate --
MAb MOC-31-PE conjugate	MAb UJ13A -- ICRT
MAb MR6 --	MAb UN3
MAb MRK-16 -- Aventis Pasteur	MAb ZME-018-gelonin conjugate
MAb MS11G6	MAB-BC2 -- GlaxoSmithKline
MAb MX-DTPA BrE-3	MAB-DM1 conjugate -- ImmunoGen
MAb MY9	MAB-ricin-chain-A conjugate -- XOMA
MAb Nd2 -- Tosoh	MAB-temoporphin conjugates
MAB NG-1 -- Hygeia	Monopharm C -- Viventia Biotech
MAB NM01 -- Nissin Food	monteplase -- Eisai
MAB OC 125	montirelin hydrate -- Gruenenthal
MAB OC 125-CMA conjugate	morotocog alfa -- Genetics Institute
MAB OKI-1 -- Ortho-McNeil	Morotocog-alfa -- Pharmacia
MAB OX52 -- Bioproducts for Science	MP 4
MAB PMA5	MP-121 -- Biopharm
MAB PR1	MP-52 -- Biopharm
MAB prost 30	MRA -- Chugai

FIG. 1T

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MS 28168 -- Mitsui Chemicals, Nihon Schering
 MSH fusion toxin -- Ligand
 MSI-99 -- Genaera
 MT 201 -- Micromet
 Muc-1 vaccine -- Corixa
 mucosal tolerance -- Aberdeen
 mullerian inhibiting subst
 muplestim -- Genetics Institute, Novartis, DSM Anti-Infectives
 murine MAB -- KS Biomedix
 Mutant somatropin -- JCR Pharmaceutical
 MV 833 -- Toagosei
 Mycoplasma pulmonis vaccine
 Mycoprex -- XOMA
 myeloperoxidase -- Henogen
 myostatin -- Genetics Institute
 Naccolomab tafenatox -- Pharmacia
 nagrestipen -- British Biotech
 NAP-5 -- Corvas Intl.
 NAPc2 -- Corvas Intl.
 nartograstim -- Kyowa
 Natalizumab -- Protein Design Labs
 Nateplase -- NIH, Nihon Schering
 nateplase -- Schering AG
 NBI-3001 -- Neurocrine Biosci.
 NBI-5788 -- Neurocrine Biosci.
 NBI-6024 -- Neurocrine Biosci.
 Nef inhibitors -- BRI
 Neisseria gonorrhoea vaccine -- Antex Biologics
 Neomycin B-arginine conjugate
 Nerelimumab -- Chiron
 Nerve growth factor -- Amgen -- Chiron, Genentech
 Nerve growth factor gene therapy
 nesiritide citrate -- Scios
 neuregulin-2 -- CeNeS
 neurocan -- NYU
 neuronal delivery system -- CAMR
 Neuroprotective vaccine -- University of Auckland
 neurotrophic chimaeras -- Regeneron
 neurotrophic factor -- NsGene, CereMedix
 NeuroVax -- Immune Response
 neuriturin -- Genentech
 neutral endopeptidase -- Genentech
 NGF enhancers -- NeuroSearch
 NHL vaccine -- Large Scale Biology
 NIP45 -- Boston Life Sciences
 NKI-B20
 NM 01 -- Nissin Food
 NMI-139 -- NitroMed
 NMMP -- Genetics Institute
 NN-2211 -- Novo Nordisk
 Noggin -- Regeneron
 Nonacog alfa
 Norelin -- Biostar
 Norwalk virus vaccine
 NRLU 10 -- NeoRx
 NRLU 10 PE -- NeoRx
 NT-3 -- Regeneron
 NT-4/5 -- Genentech
 NU 3056
 NU 3076
 NX 1838 -- Gilead Sciences
 NY ESO-1/CAG-3 antigen -- NIH
 NYVAC-7 -- Aventis Pasteur
 NZ-1002 -- Novazyme
 obesity therapy -- Nobex
 OC 10426 -- Ontogen
 OC 144093 -- Ontogen
 OCIF -- Sankyo
 Oct-43 -- Otsuka
 OK PSA - liposomal
 OKT3-gamma-1-ala-ala
 OM 991
 OM 992
 Omalizumab -- Genentech
 oncoimmunin-L -- NIH
 Oncolysin B -- ImmunoGen

FIG. 1U

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Oncolysin CD6 -- ImmunoGen
 Oncolysin M -- ImmunoGen
 Oncolysin S -- ImmunoGen
 Oncophage -- Antigenics
 Oncostatin M -- Bristol-Myers Squibb
 OncoVax-CL -- Jenner Biotherapies
 OncoVax-P -- Jenner Biotherapies
 oncept -- Yeda
 onychomycosis vaccine -- Boehringer
 Ingelheim
 opebecan -- XOMA
 opioids -- Arizona
 Oprelvekin -- Genetics Institute
 Org-33408 b-- Akzo Nobel
 Orolip DP -- EpiCept
 oryzacystatin
 OSA peptides -- GenSci Regeneration
 osteoblast-cadherin GF -- Pharis
 Osteocalcin-thymidine kinase gene therapy
 osteogenic protein -- Curis
 osteopontin -- OraPharma
 osteoporosis peptides -- Integra, Telios
 osteoprotegerin -- Amgen, SnowBrand
 otitis media vaccines -- Antex Biologics
 ovarian cancer -- University of Alabama
 OX40-IgG fusion protein -- Cantab, Xenova
 P 246 -- Diatide
 P 30 -- Alfacell
 p1025 -- Active Biotech
 P-113^A -- Demegen
 P-16 peptide -- Transition Therapeutics
 p43 -- Ramot
 P-50 peptide -- Transition Therapeutics
 p53 + RAS vaccine -- NIH, NCI
 PACAP(1-27) analogue
 paediatric vaccines -- Chiron
 Pafase -- ICOS
 PAGE-4 plasmid DNA -- IDEC
 PAI-2 -- Biotech Australia, Human
 Therapeutics
 Palivizumab -- MedImmune
 PAM 4 -- Merck
 pamiteplase -- Yamanouchi
 pancreatin, Minitabs -- Eurand
 Pangen -- Fournier
 Pantarin -- Selective Genetics
 Parainfluenza virus vaccine -- Pharmacia,
 Pierre Fabre
 paraoxanase -- Esperion
 parathyroid hormone -- Abiogen, Korea
 Green Cross
 Parathyroid hormone (1-34) --
 Chugai/Suntory
 Parkinson's disease gene therapy -- Cell
 Genesys/ Ceregene
 Parvovirus vaccine -- MedImmune
 PCP-Scan -- Immunomedics
 PDGF cocktail -- Theratechnologies
 peanut allergy therapy -- Dynavax
 PEG anti-ICAM MAb -- Boehringer
 Ingelheim
 PEG asparaginase -- Enzon
 PEG glucocerebrosidase
 PEG hirudin -- Knoll
 PEG interferon-alpha-2a -- Roche
 PEG interferon-alpha-2b + ribavirin --
 Biogen, Enzon, ICN Pharmaceuticals,
 Schering-Plough
 PEG MAb A5B7 --
 Pegacaristim -- Amgen -- Kirin Brewery --
 ZymoGenetics
 Pegaldesleukin -- Research Corp
 pegaspargase -- Enzon
 pegfilgrastim -- Amgen
 PEG-interferon Alpha -- Viragen
 PEG-interferon Alpha 2A -- Hoffman La-
 Roche
 PEG-interferon Alpha 2B -- Schering-
 Plough
 PEG-r-hirudin -- Abbott
 PEG-uricase -- Mountain View
 Pegvisomant -- Genentech

FIG. 1V

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PEGylated proteins, PolyMASC -- Valentis Pharmaprojects No. 5947 -- StressGen
 PEGylated recombinant native human leptin Pharmaprojects No. 5961 --
 -- Roche Theratechnologies
 Pentumomab Pharmaprojects No. 5962 -- NIH
 Penetratin -- Cyclacel Pharmaprojects No. 5966 -- NIH
 Pepsican -- Antisoma Pharmaprojects No. 5994 -- Pharming
 peptide G -- Peptech, ICRT Pharmaprojects No. 5995 -- Pharming
 peptide vaccine -- NIH, NCRI Pharmaprojects No. 6023 -- IMMUCON
 Pexelizumab Pharmaprojects No. 6063 -- Cytoclonal
 pexiganan acetate -- Genatera Pharmaprojects No. 6073 -- SIDDCO
 Pharmaprojects No. 3179 -- NYU Pharmaprojects No. 6115 -- Genzyme
 Pharmaprojects No. 3390 -- Ernest Orlando Pharmaprojects No. 6227 -- NIH
 Pharmaprojects No. 3417 -- Sumitomo Pharmaprojects No. 6230 -- NIH
 Pharmaprojects No. 3777 -- Acambis Pharmaprojects No. 6236 -- NIH
 Pharmaprojects No. 4209 -- XOMA Pharmaprojects No. 6243 -- NIH
 Pharmaprojects No. 4349 -- Baxter Intl. Pharmaprojects No. 6244 -- NIH
 Pharmaprojects No. 4651 Pharmaprojects No. 6281 -- Senetek
 Pharmaprojects No. 4915 -- Avanir Pharmaprojects No. 6365 -- NIH
 Pharmaprojects No. 5156 -- Rhizogenics Pharmaprojects No. 6368 -- NIH
 Pharmaprojects No. 5200 -- Pfizer Pharmaprojects No. 6373 -- NIH
 Pharmaprojects No. 5215 -- Origene Pharmaprojects No. 6408 -- Pan Pacific
 Pharmaprojects No. 5216 -- Origene Pharmaprojects No. 6410 -- Athensys
 Pharmaprojects No. 5218 -- Origene Pharmaprojects No. 6421 -- Oxford
 Pharmaprojects No. 5267 -- ML GlycoSciences
 Laboratories Pharmaprojects No. 6522 -- Maxygen
 Pharmaprojects No. 5373 -- MorphoSys Pharmaprojects No. 6523 -- Pharis
 Pharmaprojects No. 5493 -- Metabolex Pharmaprojects No. 6538 -- Maxygen
 Pharmaprojects No. 5707 -- Genentech Pharmaprojects No. 6554 -- APALEXO
 Pharmaprojects No. 5728 -- Autogen Pharmaprojects No. 6560 -- Ardana
 Pharmaprojects No. 5733 -- BioMarin Pharmaprojects No. 6562 -- Bayer
 Pharmaprojects No. 5757 -- NIH Pharmaprojects No. 6569 -- Eos
 Pharmaprojects No. 5765 -- Gryphon Phenoxazine
 Pharmaprojects No. 5830 -- AntiCancer Phenylase -- Ibex
 Pharmaprojects No. 5839 -- Dyax Pigment epithelium derived factor --
 Pharmaprojects No. 5849 -- Johnson & plasminogen activator inhibitor-1,
 Johnson recombinant -- DuPont Pharmaceuticals
 Pharmaprojects No. 5860 -- Mitsubishi-
 Tokyo
 Pharmaprojects No. 5869 -- Oxford
 GlycoSciences
 Pharmaprojects No. 5883 -- Asahi Brewery

FIG. 1W

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Plasminogen activators -- Abbott
 Laboratories, American Home Products,
 Boehringer Mannheim, Chiron
 Corporation, DuPont Pharmaceuticals, Eli
 Lilly, Shionogi, Genentech, Genetics
 Institute, GlaxoSmithKline, Hemispherx
 Biopharma, Merck & Co, Novartis,
 Pharmacia Corporation, Wakamoto, Yeda
 plasminogen-related peptides -- Bio-Tech.
 General/MGH
 platelet factor 4 -- RepliGen
 Platelet-derived growth factor -- Amgen --
 ZymoGenetics
 plusonernerin-- Hayashibara
 PMD-2850 -- Protherics
 Pneumococcal vaccine -- Antex Biologics,
 Aventis Pasteur
 Pneumococcal vaccine intranasal --
 BioChem Vaccines/Biovector
 PR1A3
 PR-39
 pralmorelin -- Kaken
 Pretarget-Lymphoma -- NeoRx
 Priliximab -- Centocor
 PRO 140 -- Progenics
 PRO 2000 -- Procept
 PRO 367 -- Progenics
 PRO 542 -- Progenics
 pro-Apo A-I -- Esperion
 prolactin -- Genzyme
 Prosaptide TX14(A) -- Bio-Tech. General
 prostate cancer antibodies -- Immunex,
 UroCor
 prostate cancer antibody therapy --
 Genentech/UroGenesys,
 Genotherapeutics
 prostate cancer immunotherapeutics -- The
 PSMA Development Company
 prostate cancer vaccine -- Aventis Pasteur,
 Zonagen, Corixa, Dendreon, Jenner
 Biotherapies, Therion Biologics
 prostate-specific antigen -- EntrelMed
 protein A -- RepliGen
 protein adhesives -- Enzon
 protein C -- Baxter Intl., PPL Therapeutics,
 ZymoGenetics
 protein C activator -- Gilead Sciences
 protein kinase R antags -- NIH
 protirelin -- Takeda
 protocadherin 2 -- Caprion
 Pro-urokinase -- Abbott, Bristol-Myers
 Squibb, Dainippon, Tosoh -- Welfide
 P-selectin glycoprotein ligand-1 -- Genetics
 Institute
 pseudomonal infections -- InterMune
 Pseudomonas vaccine -- Cytovax
 PSGL-Ig -- American Home Products
 PSP-94 -- Procyon
 PTH 1-34 -- Nobex
 QuilImmune-M -- Antigenics
 R 101933
 R 125224 -- Sankyo
 RA therapy -- Cardion
 Rabies vaccine recombinant -- Aventis
 Pasteur, BioChem Vaccines, Kaketsuken
 Pharmaceuticals
 RadioTheraCIM -- YM BioSciences
 Ramot project No. 1315 -- Ramot
 Ramot project No. K-734A -- Ramot
 Ramot project No. K-734B -- Ramot
 RANK -- Immunex
 ranpimase -- Alfacell
 ranpimase-anti-CD22 Mab -- Alfacell
 RANTES inhibitor -- Milan
 RAPID drug delivery systems -- ARIAD
 rasburicase -- Sanofi
 rBPI-21, topical -- XOMA
 RC 529 -- Corixa
 rCFTR -- Genzyme Transgenics
 RD 62198
 rDnase -- Genentech
 RDP-58 -- SangStat

FIG. 1X

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RecepTox-Fce -- Keryx	Ribozyme gene therapy -- Genset
RecepTox-GnRH -- Keryx, MTR Technologies	Rickettsial vaccine recombinant
RecepTox-MBP -- Keryx, MTR Technologies	RIGScan CR -- Neoprobe
recFSH -- Akzo Nobel, Organon	RIP-3 -- Rigel
REGA 3G12	RK-0202 -- RxKinetix
Regavirumab -- Teijin	RLT peptide -- Esperion
relaxin -- Connetics, Corp	rMNEI -- IVAX
Renal cancer vaccine -- Macropharm	rmCRP -- Immtech
repifermin -- Human Genome Sciences	RN-1001 -- Renovo
Respiratory syncytial virus PFP-2 vaccine -- Wyeth-Lederle	RN-3 -- Renovo
Respiratory syncytial virus vaccine -- GlaxoSmithKline, Pharmacia, Pierre Fabre	RNAse conjugate -- Immunomedics
Respiratory syncytial virus vaccine inactivated	RO 631908 -- Roche
Respiratory syncytial virus-parainfluenza virus vaccine -- Aventis Pasteur, Pharmacia	Rotavirus vaccine -- Merck
Reteplase -- Boehringer Mannheim, Hoffman La-Roche	RP 431 -- DuPont Pharmaceuticals
Retropep -- Retroscreen	RP-128 -- Resolution
RFB4 (dsFv) PE38	RPE65 gene therapy --
RFI 641 -- American Home Products	RPR 110173 -- Aventis Pasteur
RFTS -- UAB Research Foundation	RPR 115135 -- Aventis Pasteur
RG 12986 -- Aventis Pasteur	RPR 116258A -- Aventis Pasteur
RG 83852 -- Aventis Pasteur	rPSGL-Ig -- American Home Products
RG-1059 -- RepliGen	r-SPC surfactant -- Byk Gulden
rGCR -- NIH	rV-HER-2/neu -- Theron Biologics
rGLP-1 -- Restoragen	SA 1042 -- Sankyo
rGRF -- Restoragen	sacrosidase -- Orphan Medical
rh Insulin -- Eli Lilly	Sant 7
RHAMM targeting peptides -- Cangene	Sargramostim -- Immunex
rHb1.1 -- Baxter Intl.	saruplase -- Gruenenthal
rhCC10 -- Claragen	Satumomab -- Cytogen
rhCG -- Sero	SB 1 -- COR Therapeutics
Rheumatoid arthritis gene therapy	SB 207448 -- GlaxoSmithKline
Rheumatoid arthritis vaccine -- Veterans Affairs Medical Center	SB 208651 -- GlaxoSmithKline
rhLH -- Sero	SB 240683 -- GlaxoSmithKline
	SB 249415 -- GlaxoSmithKline
	SB 249417 -- GlaxoSmithKline
	SB 6 -- COR Therapeutics
	SB RA 31012 --
	SC 56929 -- Pharmacia
	SCA binding proteins -- Curis, Enzon
	scFv(14E1)-ETA Berlex Laboratories,
	Schering AG
	ScFv(FRP5)-ETA --

FIG. 1Y

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ScFv6C6-PE40 --
 SCH 55700 -- Celltech
 Schistosomiasis vaccine -- Glaxo
 Wellcome/Medevea, Brazil
 SCPF -- Advanced Tissue Sciences
 scuPA-suPAR complex -- Hadasit
 SD-9427 -- Pharmacia
 SDF-1 -- Ono
 SDZ 215918 -- Novartis
 SDZ 280125 -- Novartis
 SDZ 89104 -- Novartis
 SDZ ABL 364 -- Novartis
 SDZ MMA 383 -- Novartis
 serine protease inhibs -- Pharis
 semorelin acetate -- Serono
 SERP-1 -- Viron
 serteneff -- Dainippon
 serum albumin, Recombinant human --
 Aventis Behring
 serum-derived factor -- Hadasit
 Sevrumab -- Novartis
 SGN 14 -- Seattle Genetics
 SGN 15 -- Seattle Genetics
 SGN 17/19 -- Seattle Genetics
 SGN 30 -- Seattle Genetics
 SGN-10 -- Seattle Genetics
 SGN-11 -- Seattle Genetics
 SH 306 -- DuPont Pharmaceuticals
 Shanvac-B -- Shantha
 Shigella flexneri vaccine -- Avant, Acambis,
 Novavax
 Shigella sonnei vaccine --
 sICAM-1 -- Boehringer Ingelheim
 Silteplase -- Genzyme
 SIV vaccine -- Endocon, Institut Pasteur
 SK 896 -- Sanwa Kagaku Kenkyusho
 SK-827 -- Sanwa Kagaku Kenkyusho
 Skeletex -- CellFactors
 SKF 106160 -- GlaxoSmithKline
 S-nitroso-AR545C --
 SNTP -- Active Biotech
 somatomedin-1 -- GroPep, Mitsubishi-
 Tokyo, NIH
 somatomedin-1 carrier protein -- Insmed
 somatostatin -- Ferring
 Somatotropin/
 Human Growth Hormone -- Bio-Tech.
 General, Eli Lilly
 somatropin -- Bio-Tech. General, Alkermes,
 ProLease, Aventis Behring, Biovector,
 Cangene, Dong-A, Eli Lilly, Emisphere,
 Enact, Genentech, Genzyme Transgenics,
 Grandis/InfiMed, CSL, InfiMed, MacroMed,
 Novartis, Novo Nordisk, Pharmacia
 Serono, TranXenoGen
 somatropin derivative -- Schering AG
 somatropin, AIR -- Eli Lilly
 Somatropin, inhaled -- Eli Lilly/Alkermes
 somatropin, Kabi -- Pharmacia
 somatropin, Orasome -- Novo Nordisk
 Sonermin -- Dainippon Pharmaceutical
 SP(V5.2)C -- Supertek
 SPf66
 sphingomyelinase -- Genzyme
 SR 29001 -- Sanofi
 SR 41476 -- Sanofi
 SR-29001 -- Sanofi
 SS1(dsFV)-PE38 -- NeoPharm
 β 2 microglobulin -- Avidex
 β 2-microglobulin fusion proteins -- NIH
 β -amyloid peptides -- CeNeS
 β -defensin -- Pharis
 Staphylococcus aureus infections --
 Inhibitex/ZLB
 Staphylococcus aureus vaccine conjugate --
 Nabi
 Staphylococcus therapy -- Tripep
 Staphylokinase -- Biovation, Prothera,
 Thrombogenetics
 Streptococcal A vaccine -- M6
 Pharmaceuticals, North American Vaccine
 Streptococcal B vaccine -- Microscience

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Streptococcal B vaccine recombinant --
 Biochem Vaccines
 Streptococcus pyogenes vaccine
 STRL-33 -- NIH
 Subalin -- SRC VB VECTOR
 SUI5 -- United Biomedical
 SUI5-LHRH -- United Biomedical
 SUN-E3001 -- Suntory
 super high affinity monoclonal antibodies --
 YM BioSciences
 Superoxide dismutase -- Chiron, Enzon,
 Ube Industries, Bio-Tech, Yeda
 superoxide dismutase-2 -- OXIS
 suppressin -- UAB Research Foundation
 SY-161-P5 -- ThromboGenics
 SY-162 -- ThromboGenics
 Systemic lupus erythematosus vaccine --
 MedClone/VivoRx
 T cell receptor peptide vaccine
 T4N5 liposomes -- AGI Dermatics
 TACI, soluble -- ZymoGenetics
 targeted apoptosis -- Antisoma
 tasonermin -- Boehringer Ingelheim
 TASP
 TASP-V
 Tat peptide analogues -- NIH
 TBP I -- Yeda
 TBP II
 TBV25H -- NIH
 Tc 99m lor cea1 -- Center of Molecular
 Immunology
 Tc 99m P 748 -- Diatide
 Tc 99m votumumab -- Intracell
 Tc-99m rh-Annexin V -- Theseus Imaging
 teceleukin -- Biogen
 tenecteplase -- Genentech
 Teriparatide -- Armour Pharmaceuticals,
 Asahi Kasei, Eli Lilly
 terlipressin -- Ferring
 testisin -- AMRAD
 Tetrafilbricin -- Roche
 TFPI -- EntreMed
 tgD-IL-2 -- Takeda
 TGF-Alpha -- ZymoGenetics
 TGF- β -- Kolon
 TGF- β 2 -- Insmed
 TGF- β 3 -- OSI
 Thalassaemia gene therapy -- Crucell
 TheraCIM-h-R3 -- Center of Molecular
 Immunology, YM BioSciences
 Theradigm-HBV -- Epimmune
 Theradigm-HPV -- Epimmune
 Theradigm-malaria -- Epimmune
 Theradigm-melanoma -- Epimmune
 TheraFab -- Antisoma
 ThGRF 1-29 -- Theratechnologies
 ThGRF 1-44 -- Theratechnologies
 thrombomodulin -- Iowa, Novocastra
 Thrombopoietin -- Dragon Pharmaceuticals,
 Genentech
 thrombopoietin, Pliva -- Recepton
 Thrombospondin 2 --
 thrombostatin -- Thromgen
 thymalfasin -- SciClone
 thymocartin -- Gedeon Richter
 thymosin Alpha1 -- NIH
 thyroid stimulating hormone -- Genzyme
 tICAM-1 -- Bayer
 Tick anticoagulant peptide -- Merck
 TIF -- Xoma
 Tifacogin -- Chiron, NIS, Pharmacia
 Tissue factor -- Genentech
 Tissue factor pathway inhibitor
 TJN-135 -- Tsumura
 TM 27 -- Avant
 TM 29 -- Avant
 TMC-151 -- Tanabe Seiyaku
 TNF tumour necrosis factor -- Asahi Kasei
 TNF Alpha -- Cytimmune
 TNF antibody -- Johnson & Johnson
 TNF binding protein -- Amgen
 TNF degradation product -- Oncotech

FIG. 1AA

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TNF receptor -- Immunex	TXU-PAP
TNF receptor 1, soluble -- Amgen	TY-10721 -- TOA Eiyo
TNF Tumour necrosis factor-alpha -- Asahi Kasei, Genentech, Mochida	Type I diabetes vaccine -- Research Corp
TNF-Alpha inhibitor -- Tripep	Typhoid vaccine CVD 908
TNFR:Fc gene therapy -- Targeted Genetics	U 143677 -- Pharmacia
TNF-SAM2	U 81749 -- Pharmacia
Tolerimab -- Innogenetics	UA 1248 -- Arizona
Toxoplasma gondii vaccine -- GlaxoSmithKline	UGIF -- Sheffield
TP 9201 -- Telios	UIC 2
TP10 -- Avant	UK 101
TP20 -- Avant	UK-279276 -- Corvas Intl.
tPA -- Centocor	urodilatin -- Pharis
trafermin -- Scios	urofolitrophin -- Serono
TRAIL/Apo2L -- Immunex	uteroferrin -- Pepgen
transferrin-binding proteins -- CAMR	V 20 -- GLYCODEsign
Transforming growth factor-beta-1 -- Genentech	V2 vasopressin receptor gene therapy vaccines -- Active Biotech
transport protein -- Genesis	Varicella zoster glycoprotein vaccine -- Research Corporation Technologies
TRH -- Ferring	Varicella zoster virus vaccine live -- Cantab Pharmaceuticals
Triabin -- Schering AG	Vascular endothelial growth factor -- Genentech, University of California
Triconal	Vascular endothelial growth factors -- R&D Systems
Triflavin	vascular targeting agents -- Peregrine
troponin I -- Boston Life Sciences	vasopermeation enhancement agents -- Peregrine
TRP-2 ^A -- NIH	vasostatin -- NIH
trypsin inhibitor -- Mochida	VCL -- Bio-Tech. General
TSP-1 gene therapy --	VEGF -- Genentech, Scios
TT-232	VEGF inhibitor -- Chugai
TTS-CD2 -- Active Biotech	VEGF-2 -- Human Genome Sciences
Tuberculosis vaccine -- Aventis Pasteur, Genesis	VEGF-Trap -- Regeneron
Tumor Targeted Superantigens -- Active Biotech -- Pharmacia	viscumin, recombinant -- Madaus
tumour vaccines -- PhotoCure	Vitaxin
tumour-activated prodrug antibody conjugates -- Millennium/ImmunoGen	Vitrax -- ISTA Pharmaceuticals
tumstatin -- ILEX	West Nile virus vaccine -- Bavarian Nordic
Tuvirumab -- Novartis	WP 652
TV-4710 -- Teva	WT1 vaccine -- Corixa
TWEAK receptor -- Immunex	WX-293 -- Willex BioTech.

FIG. 1BB

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WX-360 -- Wilex BioTech.	YM 207 -- Yamanouchi
WX-UK1 -- Wilex BioTech.	YM 337 -- Protein Design Labs
XMP-500 -- XOMA	Yttrium-90 labelled biotin
XomaZyme-791 -- XOMA	Yttrium-90-labeled anti-CEA MAb T84.66 --
XTL 001 -- XTL Biopharmaceuticals	ZD 0490 -- AstraZeneca
XTL 002 -- XTL Biopharmaceuticals	ziconotide -- Elan
yeast delivery system -- GlobelImmune	ZK 157138 -- Berlex Laboratories
Yersinia pestis vaccine	Zollmombab aritox
YIGSR-Stealth -- Johnson & Johnson	Zorcell -- Immune Response
Yisum Project No. D-0460 -- Yisum	ZRXL peptides -- Novartis

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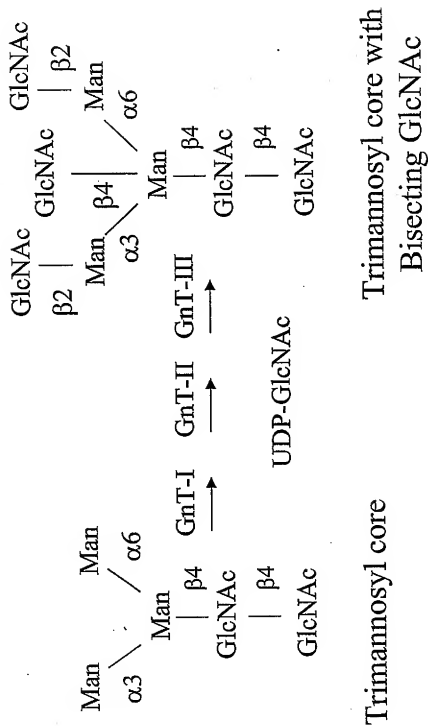
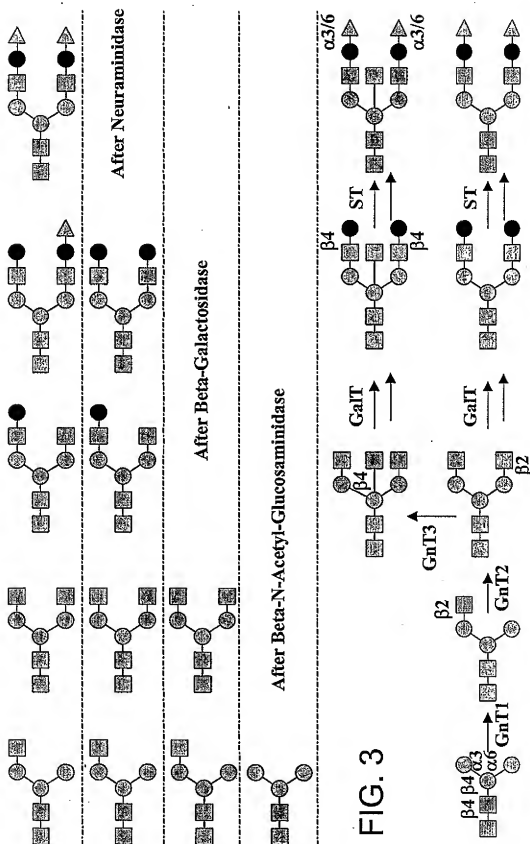


FIG. 2

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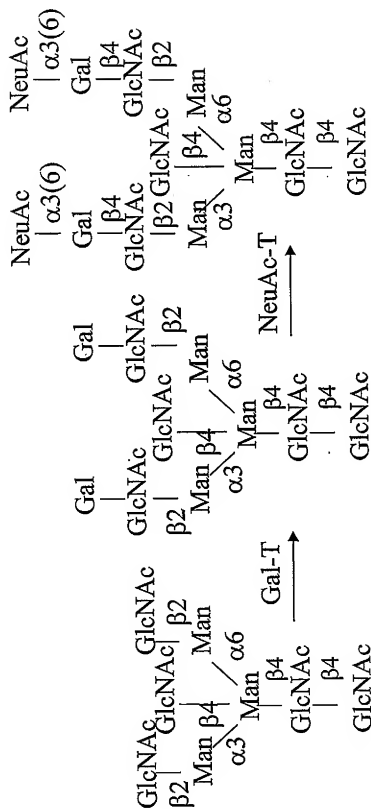


FIG. 4

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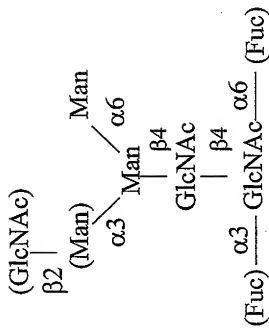


FIG. 7

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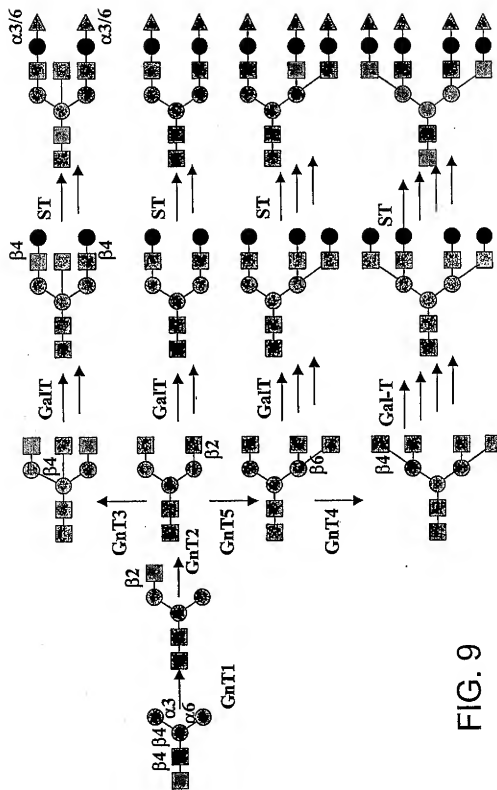


FIG. 9

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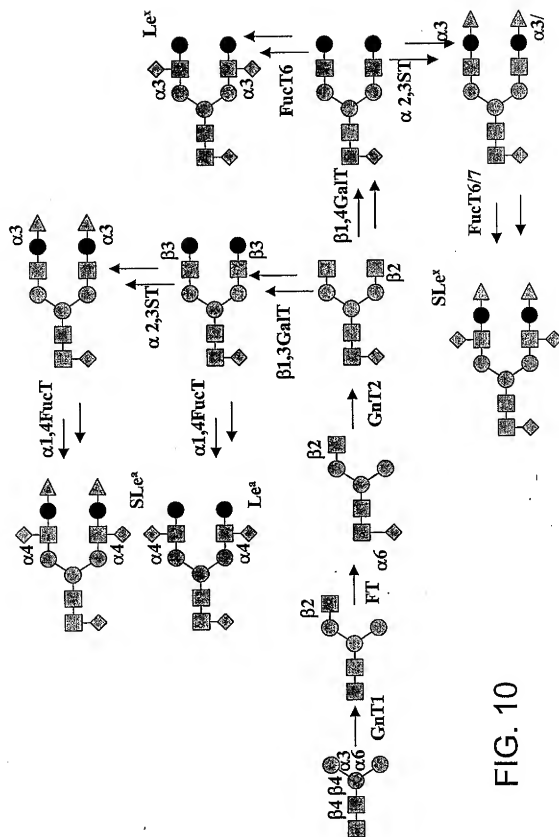


FIG. 10

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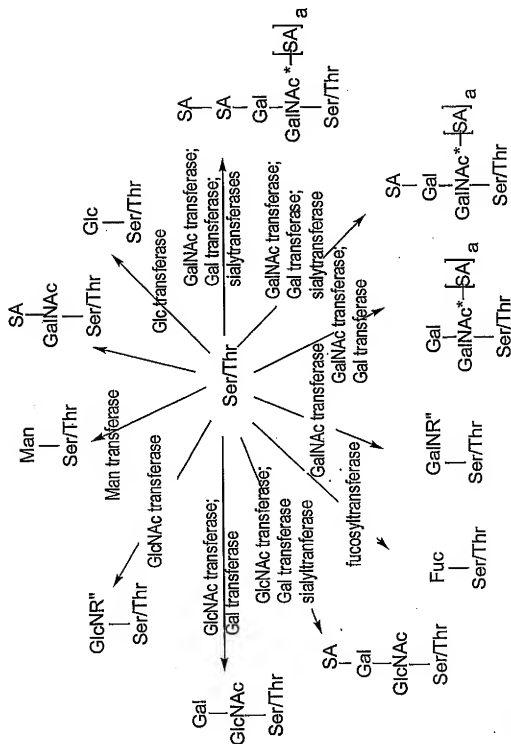


FIG. 11

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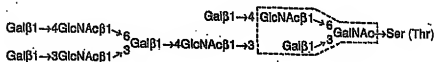
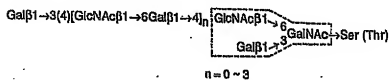
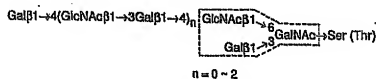
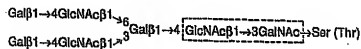
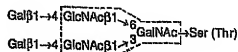
Core 1*Core 2**Core 3**Core 4*

FIG. 12

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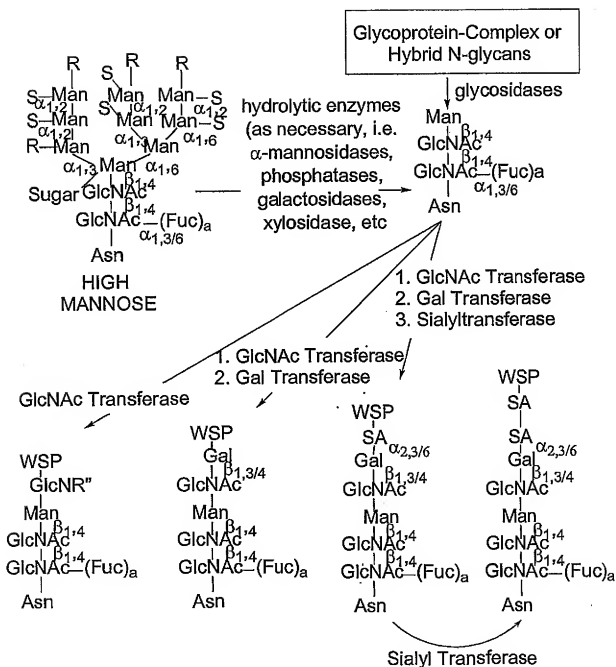


FIG. 14

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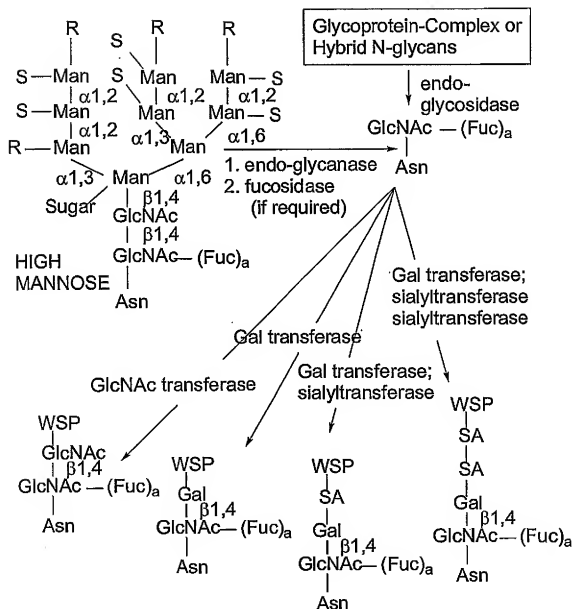


FIG. 16

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O-LINKED OLIGOSACCHARIDES

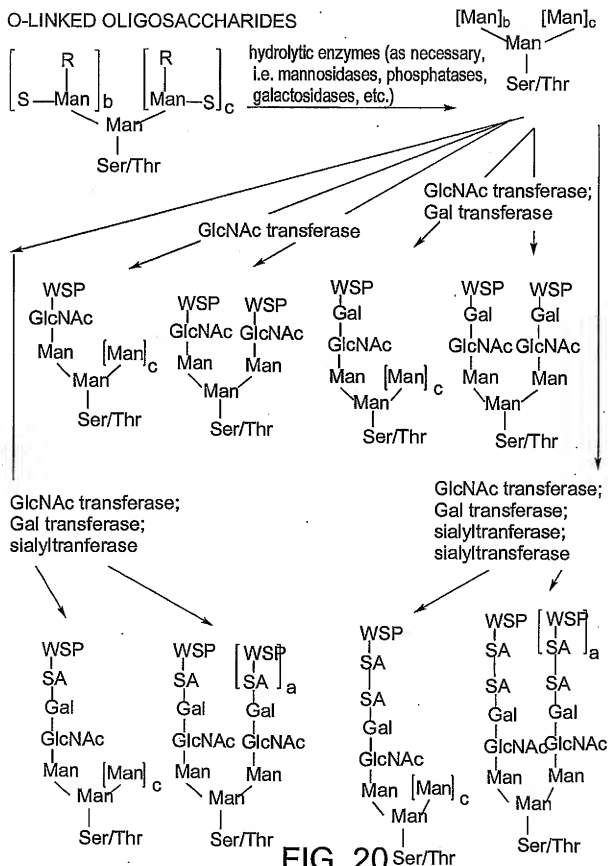
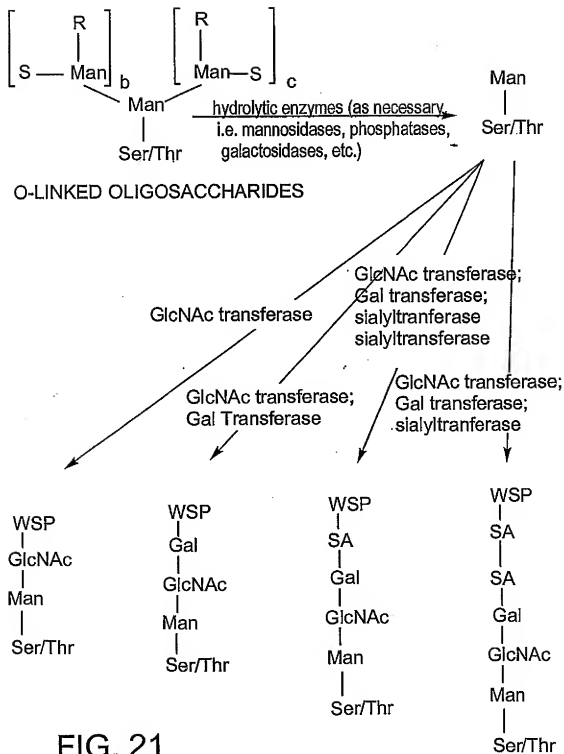


FIG. 20

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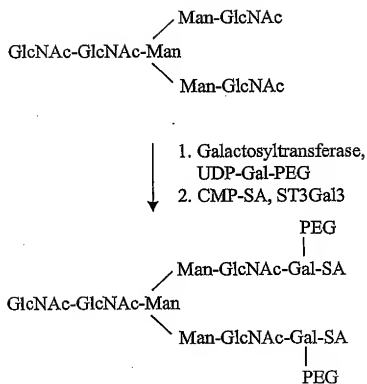


FIG. 22A

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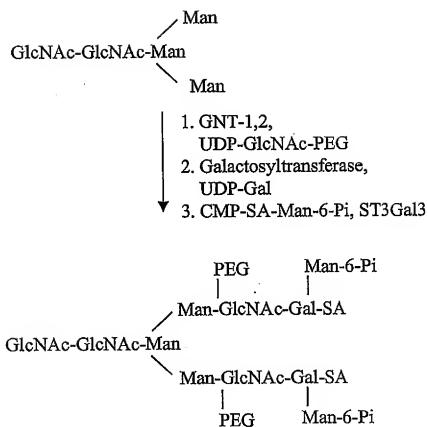


FIG. 22B

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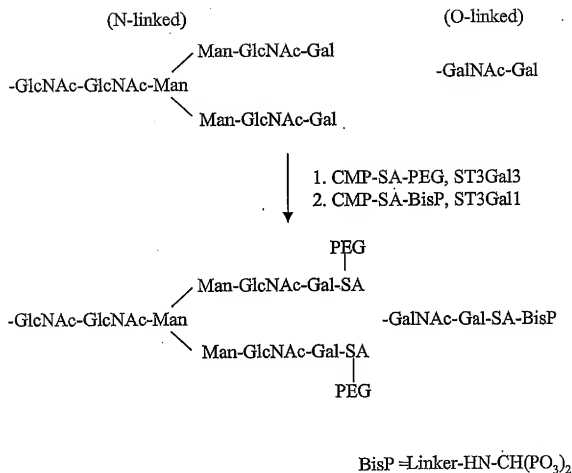


FIG. 22C

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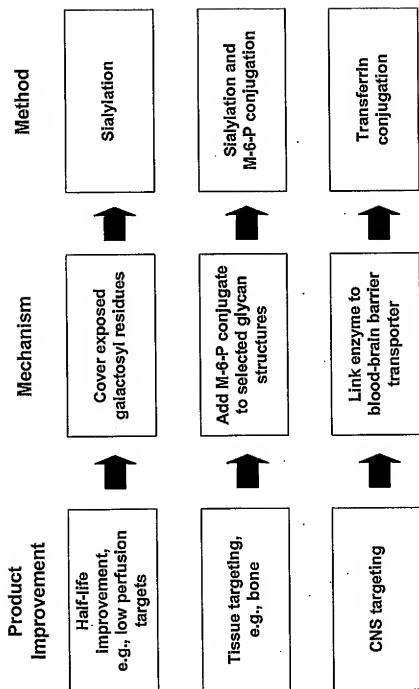


FIG. 23

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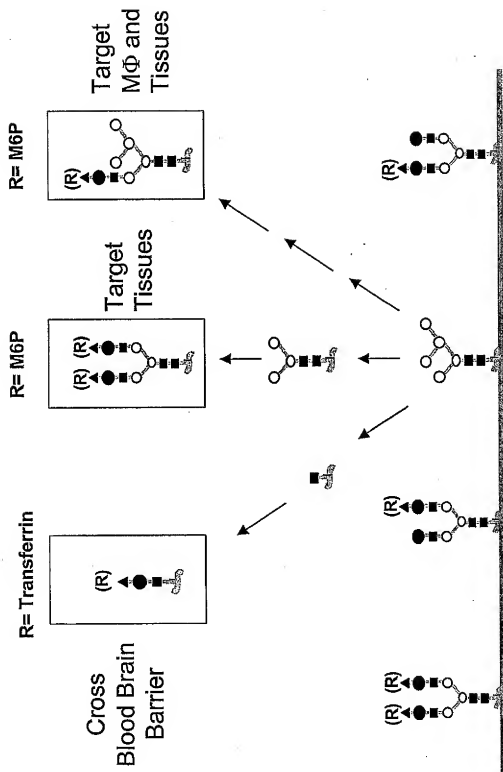


FIG. 24

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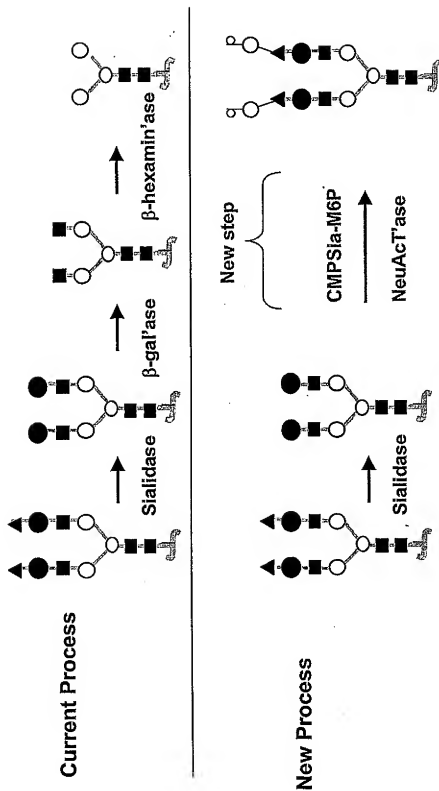


FIG. 25

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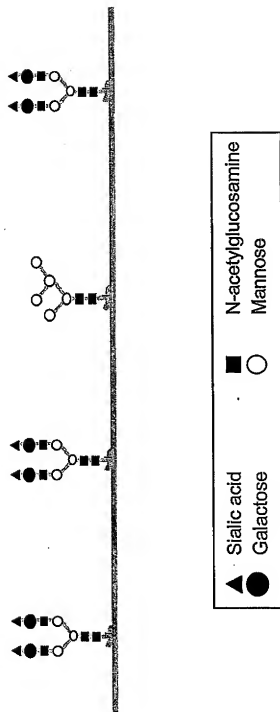
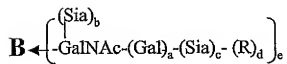
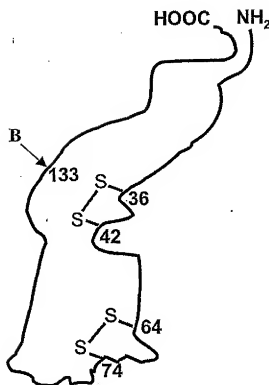


FIG. 26

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a-c, e (independently selected) = 0 or 1;

d = 0;

R = modifying group, mannose, oligo-mannose

FIG. 27A

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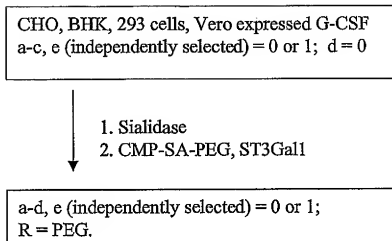


FIG. 27B

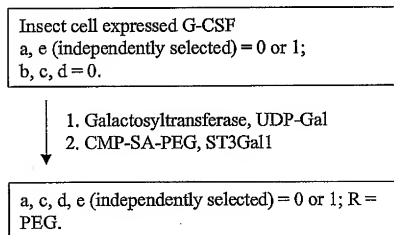


FIG. 27C

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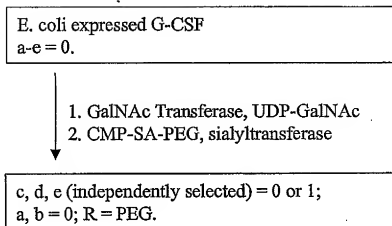


FIG. 27D

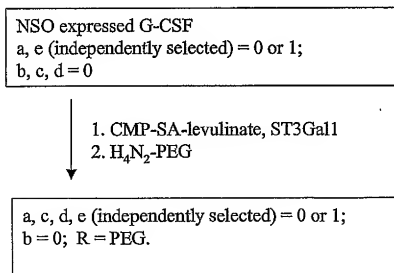


FIG. 27E

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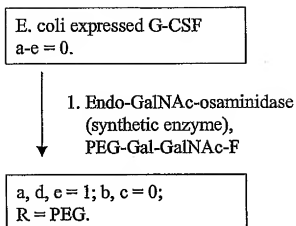


FIG. 27F

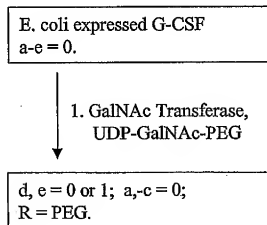
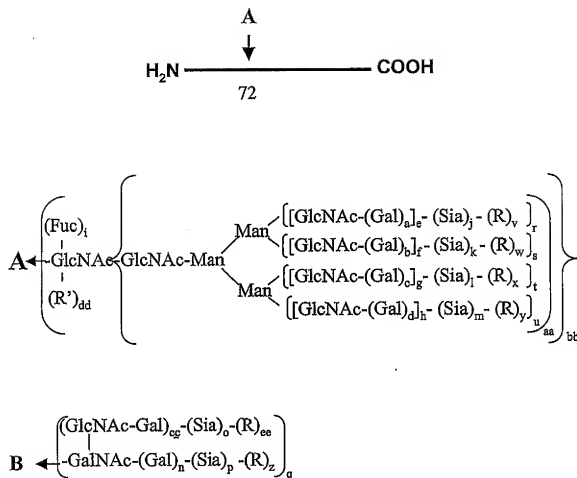


FIG. 27G

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a-d, i, n-u (independently selected) = 0 or 1.

aa, bb, cc, dd, ee (independently selected) = 0 or 1.

e-h (independently selected) = 0 to 6.

j-m (independently selected) = 0 to 20.

v-z = 0; R = modifying group, mannose, oligo-mannose.

R' = H, glycosyl residue, modifying group,

glycoconjugate.

FIG. 28A

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CHO, BHK, 293 cells, Vero expressed
interferon alpha 14C.
a-d, aa, bb = 1; e-h = 1 to 4;
cc, j-m, i, r-u (independently selected) = 0 or 1;
q, n-p, v-z, cc, dd, ee = 0.

- ↓
1. Sialidase
 2. CMP-SA-PEG, ST3Gal3

a-d, aa, bb = 1; e-h = 1 to 4;
bb, cc, i, r-u (independently selected) = 0 or 1;
q, n-p, v-z, cc, dd, ee = 0;
v-y (independently selected) = 1,
when j-m (independently selected) = 1;
R = PEG.

FIG. 28B

Insect cell or fungi expressed interferon alpha-14C.
a-d, f, h, j-q, s, u, v-z, cc, dd, ee = 0;
e, g, i, r, t (independently selected) = 0 or 1;
aa, bb = 1.

- ↓
1. GNT's 1&2, UDP-GlcNAc
 2. Galactosyltransferase, UDP-Gal-PEG

b, d, f, h, j-q, s, u, w, y, z, cc, dd, ee = 0;
a, c, e, g, i, r, t, v, x (independently selected) = 0 or 1;
v, x (independently selected) = 1,
when a, c, (independently selected) = 1;
aa, bb = 1; R = PEG.

FIG. 28C

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Yeast expressed interferon alpha-14C.

a-q, cc, dd, ee, v-z = 0;

r-y (independently selected) = 0 to 1;

aa, bb = 1;

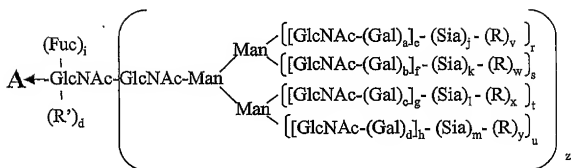
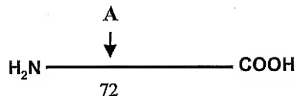
R (branched or linear) = Man, oligomannose or polysaccharide.

- ↓
1. Endo-H
 2. Galactosyltransferase, UDP-Gal
 - 3.. CMP-SA-PEG, ST3Gal3

a-z, bb = 0; aa = 1; R' = -Gal-Sia-PEG.

FIG. 28D

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a-d, i, r-u (independently selected) = 0 or 1.

e-h (independently selected) = 0 to 4.

j-m (independently selected) = 0 or 1.

n, v-y = 0; z = 0 or 1.

R = polymer; R' = sugar, glycoconjugate.

FIG. 28E

68/345

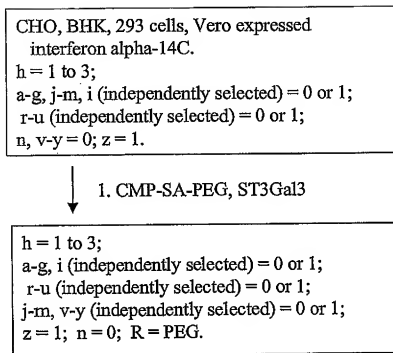


FIG. 28F

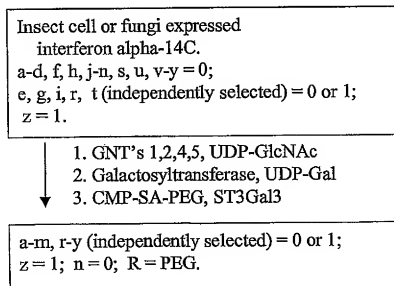


FIG. 28G

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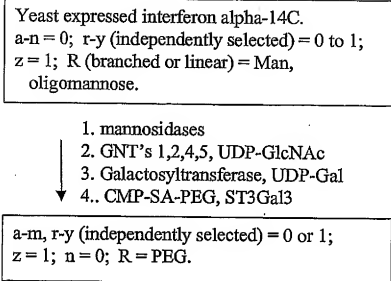


FIG. 28H

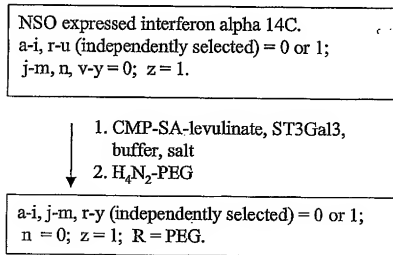


FIG. 28I

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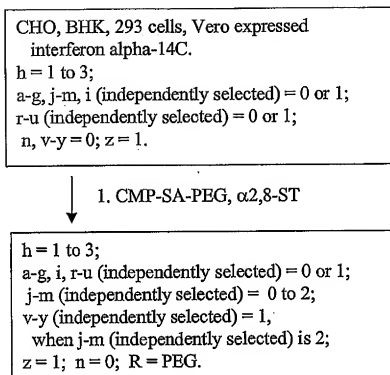


FIG. 28J

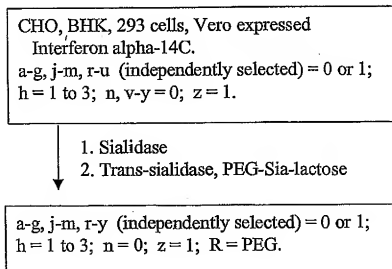


FIG. 28K

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CHO, BHK, 293 cells, Vero expressed
interferon alpha-14C.

h = 1 to 3;

a-g, j-m, i (independently selected) = 0 or 1;

r-u (independently selected) = 0 or 1;

n, v-y = 0; z = 1.

1. CMP-SA, α 2,8-ST

h = 1 to 3;

a-g, i, r-u (independently selected) = 0 or 1;

j-m (independently selected) = 0 to 40;

z = 1; v-y, n = 0.

FIG. 28L

Insect cell or fungi expressed interferon alpha-14C.

a-d, f, h, j-n, s, u, v-y = 0;

e, g, i, r, t (independently selected) = 0 or 1;

z = 1.

1. GNT's 1 & 2, UDP-GlcNAc

2. Galactosyltransferase,

UDP-Gal-linker-SA-CMP

3. ST3Gal3, transferrin

a, c, e, g, i, r, t, v, x (independently selected) = 0 or 1;

z = 1; b, d, f, h, j-n, s, u, w, y = 0;

R = transferrin.

FIG. 28M

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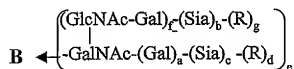
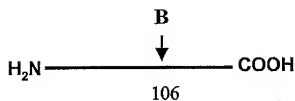
Insect cell or fungi expressed interferon alpha-14C.
a-d, f, h, j-n, s, u, v-y = 0;
e, g, i, r, t (independently selected) = 0 or 1; z = 1.

- ↓
1. endoglycanase
 2. Galactosyltransferase,
UDP-Gal-linker-SA-CMP
 3. ST3Gal3, transferrin

i (independently selected) = 0 or 1;
a-h, j-m, r-z = 0;
n = 1; R' = -Gal-linker-transferrin.

FIG. 28N

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a-c, e, f (independently selected) = 0 or 1;
 d, g = 0; R = polymer, glycoconjugate.

FIG. 280

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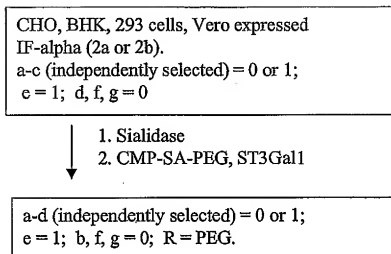


FIG. 28P

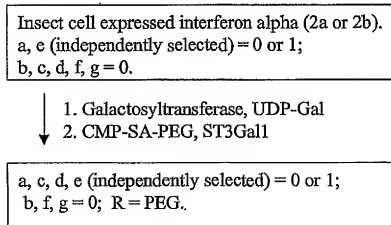


FIG. 28Q

75/345

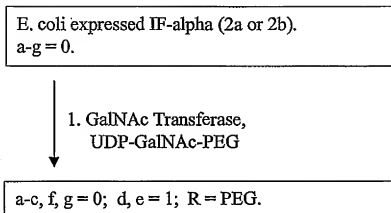


FIG. 28R

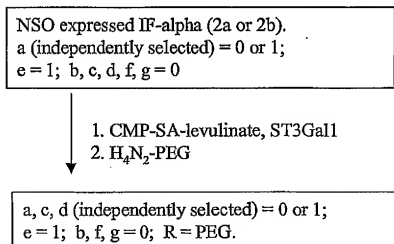


FIG. 28S

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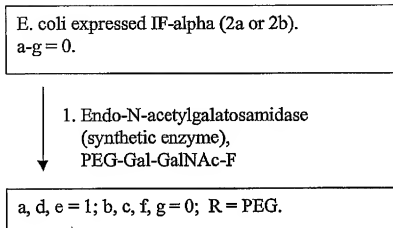


FIG. 28T

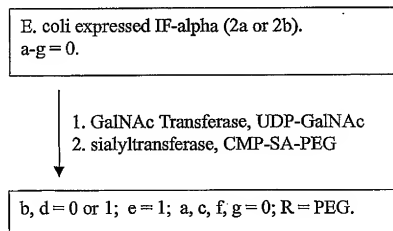


FIG. 28U

77/345

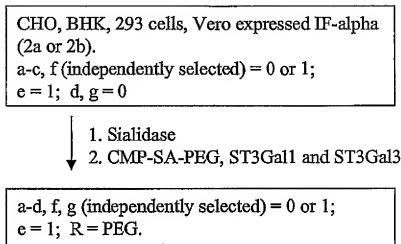


FIG. 28V

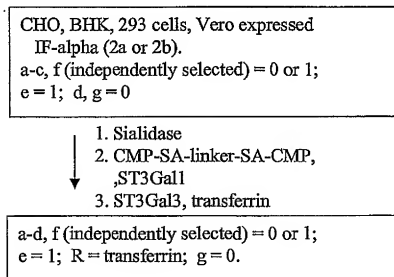
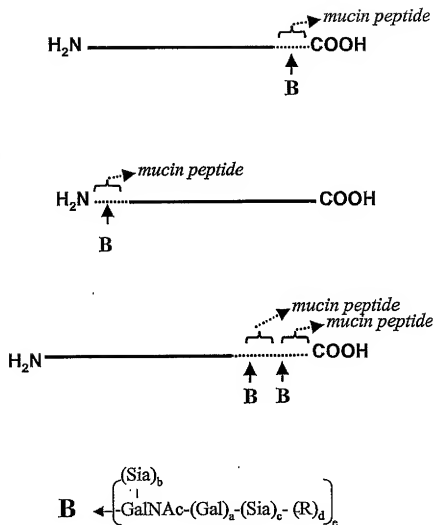


FIG. 28W

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a-c, e (independently selected) = 0 or 1;
 d = 0; R = polymer, glycoconjugate.

FIG. 28X

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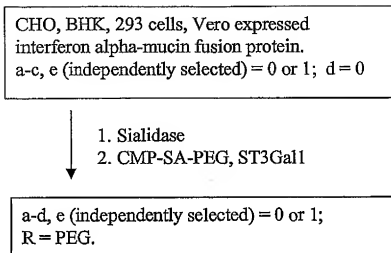


FIG. 28Y

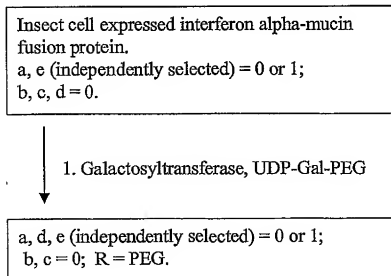


FIG. 28Z

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E. coli expressed interferon alpha-mucin
fusion protein.
a-c = 0.



1. GalNAc Transferase, UDP-GalNAc
2. CMP-SA-PEG, sialyltransferase

c, d, e (independently selected) = 0 or 1;
a, b = 0; R = PEG.

FIG. 28AA

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E. coli expressed interferon alpha-mucin
fusion protein.
a-e, n = 0.

↓
1. GalNAc Transferase,
UDP-GalNAc-PEG

d, e (independently selected) = 0 or 1;
a-c, n = 0; R = PEG.

FIG. 28CC

E. coli expressed interferon alpha-mucin fusion
protein.
a-e, n = 0.

↓
1. GalNAc Transferase,
UDP-GalNAc-linker-SA-CMP
2. ST3Gal3, asialo-transferrin
3. CMP-SA, ST3Gal3

d, e (independently selected) = 0 or 1;
a-c, n = 0; R = linker-transferrin.

FIG. 28DD

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E. coli expressed Interferon alpha (no fusion).
a-e, n = 0.

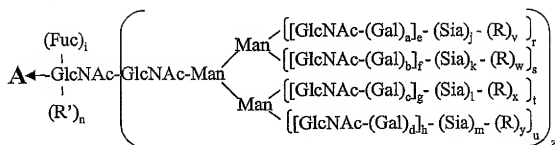


1. NHS-CO-linker-SA-CMP
2. ST3Gal3, transferrin

a-e = 0; n = 1; R' = linker-transferrin.

FIG. 28EE

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a-d, i, r-u (independently selected) = 0 or 1.

e-h (independently selected) = 0 to 4.

j-m (independently selected) = 0 or 1.

n, v-y = 0; z = 0 or 1; R = polymer

FIG. 29A

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CHO, BHK, 293 cells, Vero expressed IF-beta
 h = 1 to 3;
 a-g, j-m, i (independently selected) = 0 or 1;
 r-u (independently selected) = 0 or 1;
 n, v-y = 0; z = 1.



1. Sialidase
2. CMP-SA-PEG, ST3Gal3

h = 1 to 3;
 a-g, i (independently selected) = 0 or 1;
 r-u (independently selected) = 0 or 1;
 j-m, v-y (independently selected) = 0 or 1;
 z = 1; n = 0; R = PEG.

FIG. 29B

Insect cell expressed IF-beta
 a-d, f, h, j-n, s, u, v-y = 0;
 e, g, i, r, t (independently selected) = 0 or 1;
 z = 1.



1. GNT's 1&2, UDP-GlcNAc
2. Galactosyltransferase, UDP-Gal
3. CMP-SA-PEG, ST3Gal3,
buffer, salt

b, d, f, h, k, m, n, s, u, w, y = 0;
 a, c, e, g, i, r, t (independently selected) = 0 or 1;
 j, l, v, x (independently selected) = 0 or 1;
 z = 1; R = PEG.

FIG. 29C

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Yeast expressed IF-beta

a-n = 0; z = 1;

r-y (independently selected) = 0 to 1;

R (branched or linear) = Man, oligomannose or polysaccharide.

- ↓
1. Endo-H
 2. Galactosyltransferase, UDP-Gal
 - 3.. CMP-SA-PEG, ST3Gal3

a-m, r-z = 0; n = 1; R' = -Gal-Sia-PEG.

FIG. 29D

CHO, BHK, 293 cells, Vero expressed IF-beta

h = 1 to 3;

a-g, j-m, i (independently selected) = 0 or 1;

r-u (independently selected) = 0 or 1;

n, v-y = 0; z = 1.

- ↓
1. CMP-SA-PEG, ST3Gal3

h = 1 to 3;

a-g, i (independently selected) = 0 or 1;

r-u (independently selected) = 0 or 1;

j-m, v-y (independently selected) = 0 or 1;

z = 1; n = 0; R = PEG.

FIG. 29E

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Insect cell expressed IF-beta

a-d, f, h, j-n, s, u, v-y = 0; e, g, i, r, t
(independently selected) = 0 or 1; z = 1.

- ↓
1. GNT's 1,2,4,5, UDP-GlcNAc
 2. Galactosyltransferase, UDP-Gal
 3. CMP-SA-PEG, ST3Gal3

a-m, r-y (independently selected) = 0 or 1;
z = 1; n = 0; R = PEG.

FIG. 29F

Yeast expressed IF-beta

a-n = 0; z = 1;
r-y (independently selected) = 0 to 1;
R (branched or linear) = Man, oligomannose.

- ↓
1. mannosidases
 2. GNT's 1,2,4,5, UDP-GlcNAc
 3. Galactosyltransferase, UDP-Gal
 - 4.. CMP-SA-PEG, ST3Gal3

a-m, r-y (independently selected) = 0 or 1;
z = 1; n = 0; R = PEG.

FIG. 29G

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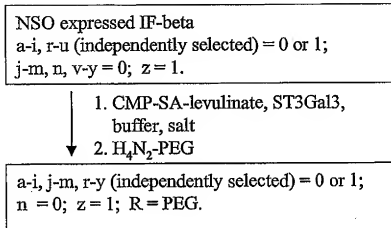


FIG. 29H

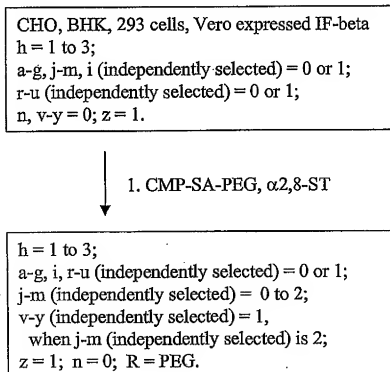


FIG. 29I

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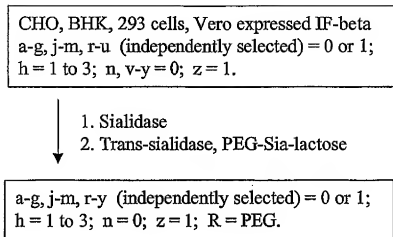


FIG. 29J

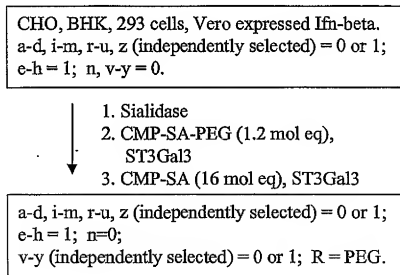


FIG. 29K

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NSO expressed Ifn-beta.

a-d, i-m, r-u, z (independently selected) = 0 or 1;

e-h = 1; n, v-y = 0;

Sia (independently selected) = Sia or Gal.

- ↓
1. Sialidase and α -galactosidase
 2. α -Galactosyltransferase, UDP-Gal
 3. CMP-SA-PEG, ST3Gal3

a-d, i-m, r-u, z (independently selected) = 0 or 1;

e-h = 1; R = PEG

n = 0; v-y (independently selected) = 1,

when j-m (independently selected) is 1;

FIG. 29L

CHO, BHK, 293 cells, Vero expressed Ifn-beta.

a-d, i-m, r-u, z (independently selected) = 0 or 1;

e-h = 1; n, v-y = 0.

- ↓
1. Sialidase
 2. CMP-SA-PEG (16 mol eq),
ST3Gal3
 3. CMP-SA, ST3Gal3

a-d, i-m, r-u, z (independently selected) = 0 or 1;

e-h = 1; n = 0;

v-y (independently selected) = 0 or 1; R = PEG.

FIG. 29M

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CHO, BHK, 293 cells, Vero expressed Ifn-beta.
a-d, i-m, r-u, z (independently selected) = 0 or 1;
e-h = 1; n, v-y = 0.

- ↓
1. CMP-SA-levulinate, ST3Gal3,
buffer, salt
 2. H₄N₂-PEG

a-d, i-m, r-u, z (independently selected) = 0 or 1;
e-h = 1; n = 0;
v-y (independently selected) = 0 or 1; R = PEG.

FIG. 29N

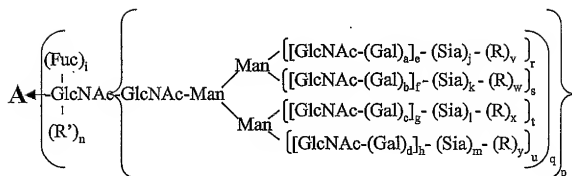
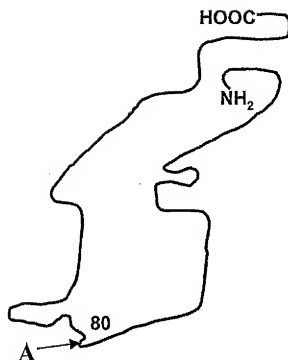
CHO, BHK, 293 cells, Vero expressed Ifn-beta.
a-d, i-m, r-u, z (independently selected) = 0 or 1;
e-h = 1; n, v-y = 0.

- ↓
1. CMP-SA, α 2,8-ST

a-d, i, r-u, z (independently selected) = 0 or 1;
e-h = 1; j-m (independently selected) = 0-20;
n, v-y (independently selected) = 0.

FIG. 29O

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a-d, i, p-u (independently selected) = 0 or 1.

e-h (independently selected) = 0 to 6.

j-m (independently selected) = 0 to 100.

v-y = 0; R = modifying group;

R' = H, glycosyl group, modifying group,
glycoconjugate.

FIG. 29P

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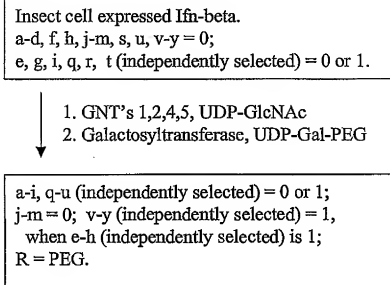


FIG. 29Q

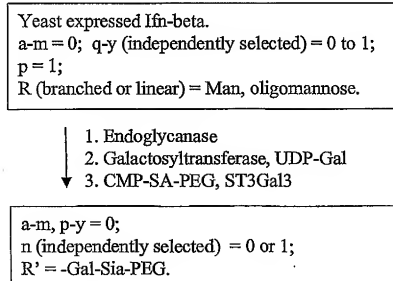


FIG. 29R

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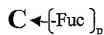
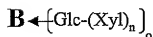
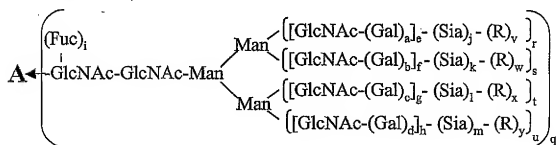
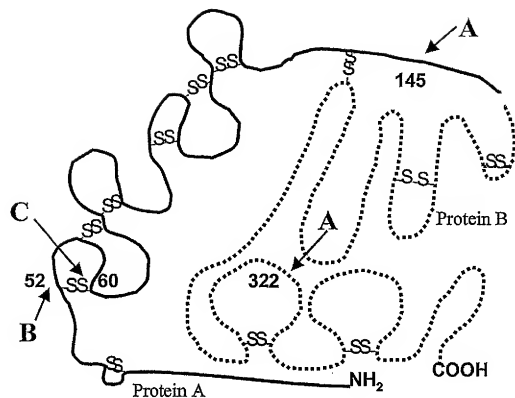
CHO, BHK, 293 cells, Vero expressed Ifn-beta.
a-d, i-m, q-u (independently selected) = 0 or 1;
e-h = 1; v-y = 0.

- ↓
1. CMP-SA-linker-SA-CMP,
ST3Gal3
 2. ST3Gal3, desialylated transferrin.
 3. CMP-SA, ST3Gal3

a-m, q-u (independently selected) = 0 or 1;
p = 1; n = 0;
v-y (independently selected) = 0 or 1;
R = linker-transferrin.

FIG. 29S

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a-d, i, q-u (independently selected) = 0 or 1.

o, p (independently selected) = 0 or 1.

e-h, n (independently selected) = 0 to 6.

j-m (independently selected) = 0 to 20.

v-y = 0;

R = modifying group, mannose, oligo-mannose, Sia-Lewis X, Sia-Lewis A.

FIG. 30A

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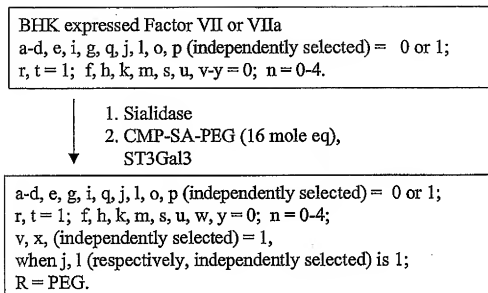


FIG. 30B

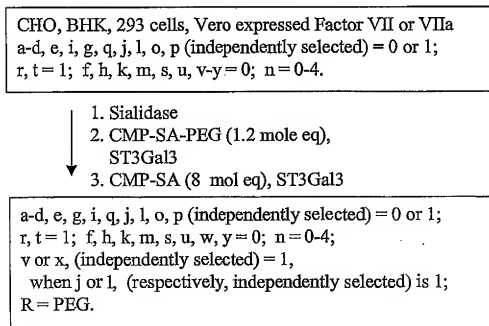


FIG. 30C

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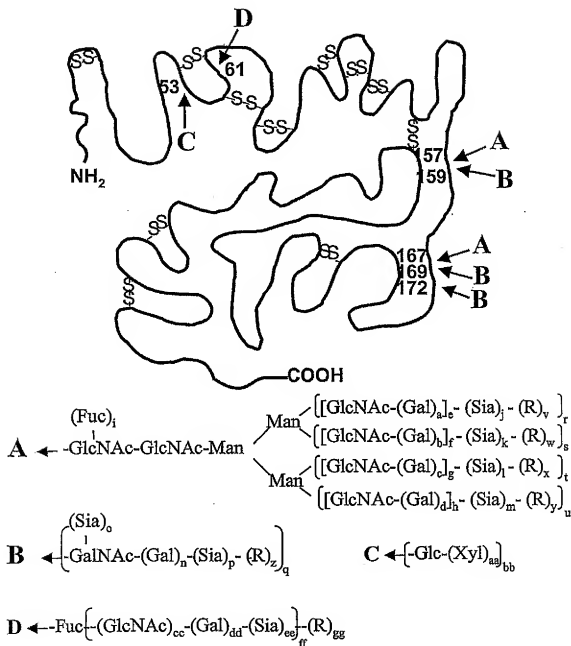
NSO expressed Factor VII or VIIa
a--u (independently selected) = 0 or 1;
v-y = 0; n = 0-4;
Sia (independently selected) = Sia or Gal.

- ↓
1. Sialidase and α -galactosidase
2. Galactosyltransferase, UDP-Gal
▼ 3. CMP-SA-PEG, ST3Gal3

a-m, o-u (independently selected) = 0 or 1;
n = 0-4; v-y (independently selected) = 1,
when j-m (independently selected) is 1;
Sia = Sia; R = PEG.

FIG. 30D

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a-d, i, n-u (independently selected) = 0 or 1.

bb, cc, dd, ee, ff, gg (independently selected) = 0 or 1.

e-h, aa (independently selected) = 0 to 6.

j-m (independently selected) = 0 to 20.

v-z = 0; R = modifying group, mannose, oligo-mannose.

FIG. 31A

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CHO, BHK, 293 cells, Vero expressed Factor IX
 a-d, q = 1; e-h = 1 to 4;
 aa, bb, cc, dd, ee, ff, j-m, i, n, o, p, r-u (independently
 selected) = 0 or 1;
 v-z, gg = 0.

- ↓
1. Sialidase
 2. CMP-SA-PEG, ST3Gal3

a-d, q = 1; e-h = 1 to 4;
 aa, bb, cc, dd, ee, ff, i, n, r-u (independently selected)
 = 0 or 1;
 o, p, z = 0;
 j-m, ee, v-y, gg (independently selected) = 0 or 1;
 R = PEG.

FIG. 31B

CHO, BHK, 293 cells, Vero expressed Factor IX
 a-d, n, q = 1; e-h = 1 to 4;
 aa, bb, cc, dd, ee, ff, j-m, i, o, p, r-u (independently
 selected) = 0 or 1;
 v-z, gg = 0.

- ↓
1. Sialidase
 2. CMP-SA-PEG, ST3Gal3
 3. ST3Gal1, CMP-SA

a-d, n, p, q = 1; e-h = 1 to 4;
 aa, bb, cc, dd, ee, ff, i, r-u (independently selected) =
 0 or 1;
 j-m, ee, v-y, gg (independently selected) = 0 or 1;
 o, z = 0; R = PEG.

FIG. 31C

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CHO, BHK, 293 cells, Vero expressed Factor IX

a-d, n, q, bb, cc, dd, ff = 1; e-h, aa = 1 to 4; ee, j-m, i, o, p, r-u (independently selected) = 0 or 1; v-z, gg = 0.

1. sialidase
2. Galactosyltransferase, UDP-Gal
3. CMP-SA, ST3Gal3
4. CMP-SA-PEG, ST3Gal1

a-d, n, q = 1; e-h = 1 to 4;

aa, bb, cc, dd, ee, ff, i, r-u (independently selected) = 0 or 1; R = PEG;

o, v-y, gg = 0;

j-m, p, ee (independently selected) = 0 or 1, but when p = 1, z = 1.

FIG. 31D

CHO, BHK, 293 cells, Vero expressed Factor IX

a-d, q = 1; e-h = 1 to 4;

aa, bb, cc, dd, ee, ff, j-m, i, n, o, p, r-u (independently selected) = 0 or 1;

v-z, gg = 0.

CMP-SA-PEG, ST3Gal3

a-d, q = 1; e-h = 1 to 4;

aa, bb, cc, dd, ee, ff, i, n, r-u (independently selected) = 0 or 1; R = PEG;

o, p, z = 0; j-m, ee, v-y, gg (independently selected) = 0 or 1.

FIG. 31E

101/345

CHO, BHK, 293 cells, Vero expressed Factor IX
 a-d, q = 1; e-h = 1 to 4;
 aa, bb, cc, dd, ee, ff, j-m, i, n, o, p, r-u (independently
 selected) = 0 or 1;
 v-z, gg = 0.

- ↓
1. CMP-SA-levulinate, ST3Gal3,
buffer, salt
 2. H₄N₂-PEG

a-d, q = 1; e-h = 1 to 4;
 aa, bb, cc, dd, ee, ff, i, n, r-u (independently selected)
 = 0 or 1;
 o, p, z = 0; R = PEG;
 j-m, ee, v-y, gg (independently selected) = 0 or 1.

FIG. 31F

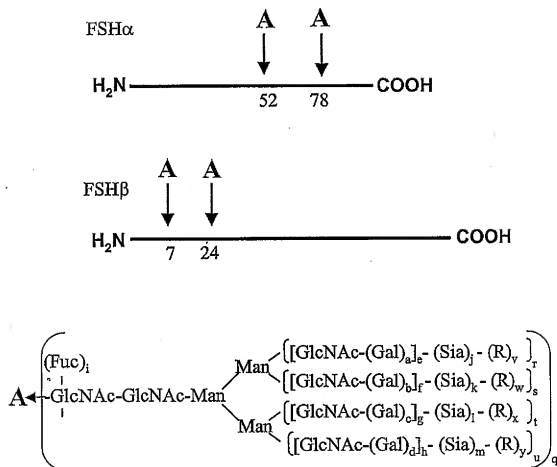
CHO, BHK, 293 cells, Vero expressed Factor IX
 a-d, n, q, bb, cc, dd, ff = 1;
 e-h, aa = 1 to 4;
 ee, j-m, i, o, p, r-u (independently selected) = 0 or 1;
 v-z, gg = 0.

- ↓
1. CMP-SA-PEG, α 2,8-ST

a-d, q = 1; e-h = 1 to 4;
 aa, bb, cc, dd, ee, ff, i, n, r-u (independently selected)
 = 0 or 1;
 o, p, z = 0; R = PEG;
 j-m, ee (independently selected) = 0 to 2;
 v-y, gg (independently selected) = 1, when j-m
 (independently selected) is 2;

FIG. 31G

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a-d, i, q-u (independently selected) = 0 or 1.

e-h (independently selected) = 0 to 6.

j-m (independently selected) = 0 to 100.

v-y = 0;

R = modifying group, mannose, oligo-mannose.

FIG. 32A

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CHO, BHK, 293 cells, Vero expressed FSH.
a-d, i-m, q-u (independently selected) = 0 or 1;
e-h = 1; v-y = 0.

- ↓
1. Sialidase
 2. CMP-SA-PEG (16 mol eq),
ST3Gal3

a-d, i-m, q-u (independently selected) = 0 or 1;
e-h = 1; v-y (independently selected) = 1,
when j-m (independently selected) is 1;
R = PEG.

FIG. 32B

CHO, BHK, 293 cells, Vero expressed FSH.
a-d, i-m, q-u (independently selected) = 0 or 1;
e-h = 1; v-y = 0.

- ↓
1. Sialidase
 2. CMP-SA-PEG (1.2 mol eq),
ST3Gal3
 3. CMP-SA (16 mol eq), ST3Gal3

a-d, i-m, q-u (independently selected) = 0 or 1;
e-h = 1; v-y (independently selected) = 0 or 1;
R = PEG.

FIG. 32C

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NSO expressed FSH.

a-d, i-m, q-u (independently selected) = 0 or 1;

e-h = 1; v-y = 0;

Sia (independently selected) = Sia or Gal.

1. Sialidase and α -galactosidase
2. Galactosyltransferase, UDP-Gal
- ▼ 3. CMP-SA-PEG, ST3Gal1

a-d, i-m, q-u (independently selected) = 0 or 1;

e-h = 1; v-y (independently selected) = 1,

when j-m (independently selected) is 1;

R = PEG.

FIG. 32D

CHO, BHK, 293 cells, Vero expressed FSH.

a-d, i-m, q-u (independently selected) = 0 or 1;

e-h = 1; v-y = 0.

1. Sialidase
2. CMP-SA-PEG (16 mol eq),
ST3Gal3
- ▼ 3. CMP-SA, ST3Gal3

a-d, i-m, q-u (independently selected) = 0 or 1;

e-h = 1; v-y (independently selected) = 0 or 1;

R = PEG.

FIG. 32E

105/345

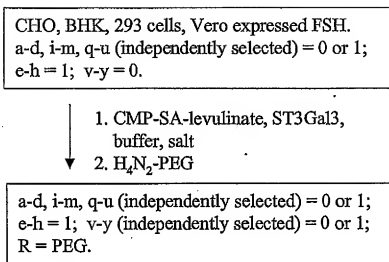


FIG. 32F

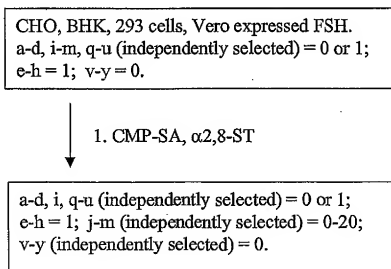


FIG. 32G

106/345

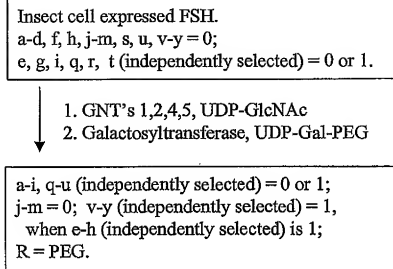


FIG. 32H

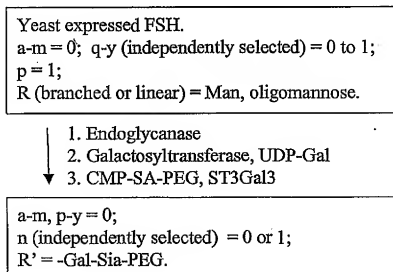


FIG. 32I

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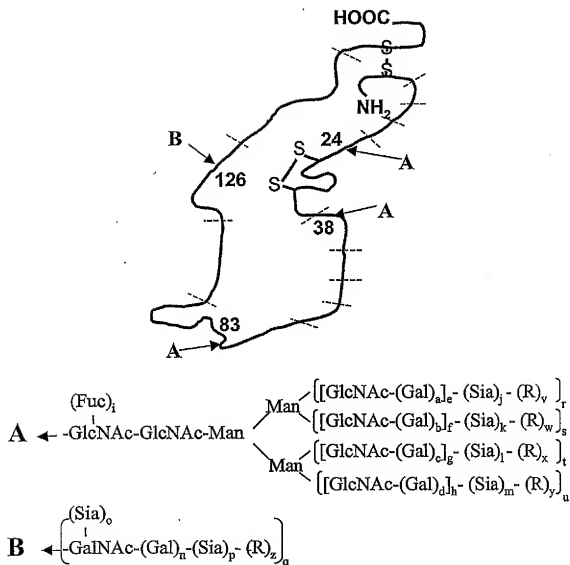
CHO, BHK, 293 cells, Vero expressed FSH.
a-d, i-m, q-u (independently selected) = 0 or 1;
e-h = 1; v-y = 0.

- ↓
1. CMP-SA-linker-SA-CMP, ST3Gal3
 2. ST3Gal1, desialylated chorionic gonadotrophin (CG) produced in CHO.
 3. CMP-SA, ST3Gal3, ST3Gal1

a-m, q-u (independently selected) = 0 or 1;
p = 1; n = 0;
v-y (independently selected) = 0 or 1;
R = linker-CG.

FIG. 32J

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a-d, i, n-u (independently selected) = 0 or 1.

e-h (independently selected) = 0 to 4.

j-m (independently selected) = 0 to 20.

v-z = 0;

R = modifying group, mannose, oligo-mannose.

FIG. 33A

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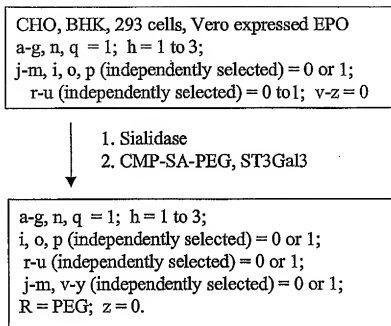


FIG. 33B

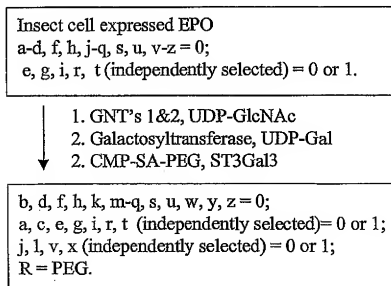


FIG. 33C

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CHO, BHK, 293 cells, Vero expressed EPO
 a-q, r-u (independently selected) = 0 or 1;
 v-z = 0.

- ↓
1. sialidase
 2. Galactosyltransferase, UDP-Gal
 3. CMP-SA, ST3Gal3
 4. CMP-SA-PEG, ST3Gal1

a-h, n, q = 1;
 i-m, o, r-u (independently selected) = 0 or 1;
 v-y = 0; p, z = 0 or 1; R = PEG.

FIG. 33D

CHO, BHK, 293 cells, Vero expressed EPO
 a-g, n, q = 1; h = 1 to 3;
 j-m, i, o, p (independently selected) = 0 or 1;
 r-u (independently selected) = 0 or 1;
 v-z = 0

- ↓
1. CMP-SA-PEG, ST3Gal3

a-g, n, q = 1; h = 1 to 3;
 i, o, p (independently selected) = 0 or 1;
 r-u (independently selected) = 0 to 1;
 j-m, v-y (independently selected) = 0 or 1;
 R = PEG; z = 0.

FIG. 33E

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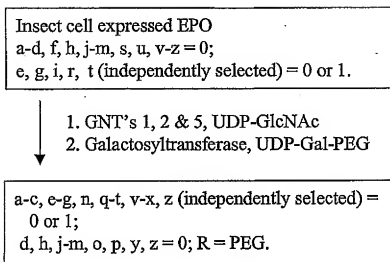


FIG. 33F

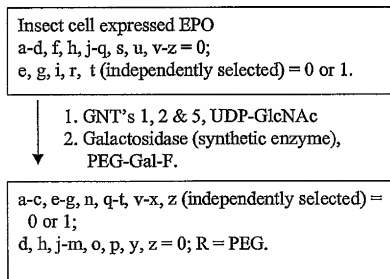


FIG. 33G

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NSO expressed NESP

q = 1; a-i, n, r-u (independently selected) = 0
or 1; j-m, o, p, v-z = 0

- ↓
1. CMP-SA-levulinate, ST3Gal3,
buffer, salt
 2. H₄N₂-PEG

q = 1; a-i, j-n, r-y (independently selected) =
0 or 1;
o, p, z = 0; R = PEG.

FIG. 33H

CHO, BHK, 293 cells, Vero expressed NESP

a-g, n, q = 1; h = 1 to 3;
j-m, i, o, p (independently selected) = 0 or 1;
r-u (independently selected) = 0 or 1;
v-z = 0

- ↓
1. CMP-SA-PEG, α 2,8-ST

a-g, n, q = 1; h = 1 to 3;
i, o, p (independently selected) = 0 or 1;
r-u (independently selected) = 0 to 1;
j-m (independently selected) = 0 to 2;
v-y (independently selected) = 1,
when j-m (independently selected) is 2;
R = PEG; z = 0.

FIG. 33I

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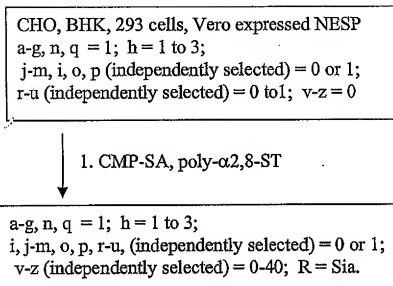
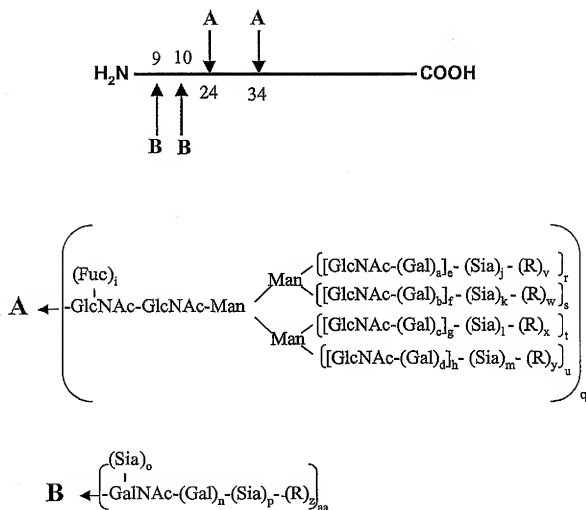


FIG. 33J

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a-d, i, n-u, aa (independently selected) = 0 or 1.

e-h (independently selected) = 0 to 6.

j-m (independently selected) = 0 to 100.

v-y = 0; R = polymer, glycoconjugate.

FIG. 34A

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CHO, BHK, 293 cells, Vero expressed GM-CSF.
 a-d, i-m, o-u, aa (independently selected) = 0 or 1;
 n, e-h = 1; v-z = 0.

- ↓
1. Sialidase
 2. CMP-SA-PEG (16 mol eq),
ST3Gal3

a-d, i-m, q-u, aa (independently selected) = 0 or 1;
 o, p, z = 0; n, e-h = 1;
 v-y (independently selected) = 1,
 when j-m (independently selected) is 1;
 R = PEG.

FIG. 34B

CHO, BHK, 293 cells, Vero expressed GM-CSF.
 a-d, i-m, o-u, aa (independently selected) = 0 or 1;
 n, e-h = 1; v-z = 0.

- ↓
1. Sialidase
 2. CMP-SA-PEG (1.2 mol eq),
ST3Gal3
 - ↓ 3. CMP-SA (16 mol eq), ST3Gal3 &
ST3Gal1

a-d, i-m, p-u, aa (independently selected) = 0 or 1;
 o, z = 0; n, e-h = 1;
 v-y (independently selected) = 0 or 1; R = PEG.

FIG. 34C

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NSO expressed GM-CSF.

a-d, i-m, o-u, aa (independently selected) = 0 or 1;

n, e-h = 1; v-z = 0;

Sia (independently selected) = Sia or Gal.

- ↓
1. Sialidase and α -galactosidase
 2. CMP-SA, ST3Gal3
 - ▼ 2. CMP-SA-PEG, ST3Gal1

a-d, i-m, p-u, z, aa (independently selected) = 0 or 1;

n, e-h = 1; o, v-y = 0; z = 1, when p = 1; R = PEG.

FIG. 34D

CHO, BHK, 293 cells, Vero expressed GM-CSF.

a-d, i-m, o-u, aa (independently selected) = 0 or 1;

n, e-h = 1; v-z = 0.

- ↓
1. Sialidase
 2. CMP-SA-PEG (16 mol eq),
ST3Gal3
 - ▼ 3. CMP-SA, ST3Gal3

a-d, i-m, q-y, aa (independently selected) = 0 or 1;

o, p, z = 0; n, e-h = 1; R = PEG.

FIG. 34E

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CHO, BHK, 293 cells, Vero expressed GM-CSF.
a-d, i-m, o-u, aa (independently selected) = 0 or 1;
n, e-h = 1; v-z = 0.



1. CMP-SA-levulinate, ST3Gal3,
buffer, salt
2. H₄N₂-PEG

a-d, i-m, o-y, aa (independently selected) = 0 or 1;
z = 0; n, e-h = 1; R = PEG.

FIG. 34F

CHO, BHK, 293 cells, Vero expressed GMCSF.
a-d, i-m, o-u, aa (independently selected) = 0 or 1;
n, e-h = 1; v-z = 0.

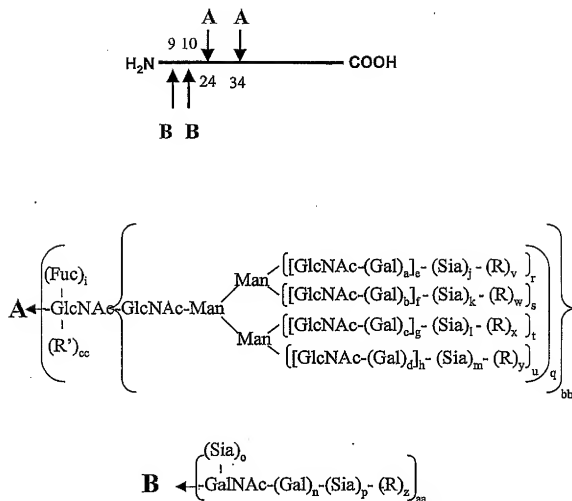


1. CMP-SA, α 2,8-ST

a-d, i, o-u, aa (independently selected) = 0 or 1;
n, e-h = 1; j-m (independently selected) = 0-20;
v-z (independently selected) = 0.

FIG. 34G

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a-d, i, n-u, aa, bb, cc (independently selected) = 0 or 1.

e-h (independently selected) = 0 to 6.

j-m (independently selected) = 0 to 100.

v-y = 0; R = modifying group, mannose, oligo-mannose.

R' = H, glycosyl residue, modifying group, glycoconjugate.

FIG. 34H

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Insect cell expressed GM-CSF.

a-d, f, h, j-m, o, p, s, u, v-z = 0;

e, g, i, n, q, r, t, aa (independently selected) = 0 or 1.

- ↓
1. GNT's 1,2,4,5, UDP-GlcNAc
 2. Galactosyltransferase, UDP-Gal-PEG

a-i, n, q-u (independently selected) = 0 or 1;

j-m = 0; v-y (independently selected) = 1,

when e-h (independently selected) is 1;

R = PEG.

FIG. 34I

Yeast expressed GM-CSF.

a-p, z, cc = 0;

q-y, aa (independently selected) = 0 to 1;

bb = 1; R (branched or linear) = Man, oligomannose;

GalNAc = Man.

- ↓
1. Endoglycanase
 2. mannosidase (if aa = 1).
 3. Galactosyltransferase, UDP-Gal-PEG

a-p, r-z, aa, bb = 0;

q, cc (independently selected) = 0 or 1;

R' = -Gal-PEG.

FIG. 34J

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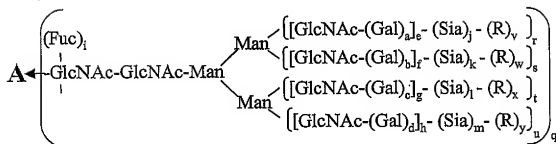
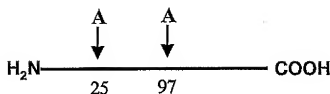
CHO, BHK, 293 cells, Vero expressed GM-CSF.
a--m, o-u, aa, bb (independently selected) = 0 or 1;
n, v-z, cc = 0.

- ↓
1. sialidase
 2. CMP-SA, ST3Gal3
 2. CMP-SA-linker-SA-CMP, ST3Gal1
 3. ST3Gal3, transferrin

a--m, p-u, z, aa (independently selected) = 0 or 1;
o, v-y, cc = 0; bb, n = 1; R = transferrin.

FIG. 34K

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a-d, i, q-u (independently selected) = 0 or 1.

e-h (independently selected) = 0 to 6.

j-m (independently selected) = 0 to 100.

v-y = 0; R = polymer.

FIG. 35A

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CHO, BHK, 293 cells, Vero expressed IF-gamma.
a-d, i-m, q-u (independently selected) = 0 or 1;
e-h = 1; v-y = 0.

- ↓
1. Sialidase
 2. CMP-SA-PEG (16 mol eq),
ST3Gal3

a-d, i-m, q-u (independently selected) = 0 or 1;
e-h = 1; v-y (independently selected) = 1,
when j-m (independently selected) is 1;
R = PEG.

FIG. 35B

CHO, BHK, 293 cells, Vero expressed IF-gamma.
a-d, i-m, q-u (independently selected) = 0 or 1;
e-h = 1; v-y = 0.

- ↓
1. Sialidase
 2. CMP-SA-PEG (1.2 mol eq),
ST3Gal3
 3. CMP-SA (16 mol eq), ST3Gal3

a-d, i-m, q-u (independently selected) = 0 or 1;
e-h = 1; v-y (independently selected) = 0 or 1;
R = PEG.

FIG. 35C

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NSO expressed Interferon gamma.

a-d, i-m, q-u (independently selected) = 0 or 1;

e-h = 1; v-y = 0;

Sia (independently selected) = Sia or Gal.

- ↓
1. Sialidase and α -galactosidase
 2. α -Galactosyltransferase, UDP-Gal
 3. CMP-SA-PEG, ST3Gal3
- ↓

a-d, i-m, q-u (independently selected) = 0 or 1;

e-h = 1; v-y (independently selected) = 1,

when j-m (independently selected) is 1;

R = PEG.

FIG. 35D

CHO, BHK, 293 cells, Vero expressed
Interferon gamma.

a-d, i-m, q-u (independently selected) = 0 or 1;

e-h = 1; v-y = 0.

- ↓
1. Sialidase
 2. CMP-SA-PEG (16 mol eq),
ST3Gal3
 3. CMP-SA, ST3Gal3
- ↓

a-d, i-m, q-u (independently selected) = 0 or 1;

e-h = 1; v-y (independently selected) = 0 or 1;

R = PEG.

FIG. 35E

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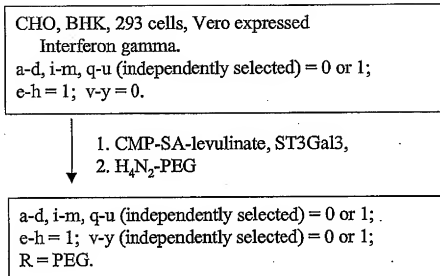


FIG. 35F

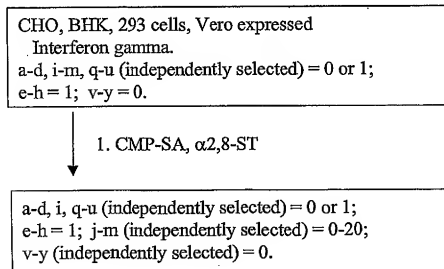
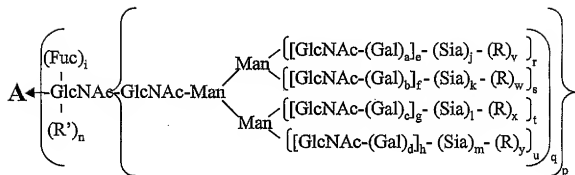
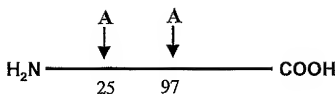


FIG. 35G

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a-d, i, n, p-u (independently selected) = 0 or 1.

e-h (independently selected) = 0 to 6.

j-m (independently selected) = 0 to 100.

v-y = 0;

R = modifying group, mannose, oligo-mannose;

R' = H, glycosyl residue, modifying group,
glycoconjugate.

FIG. 35H

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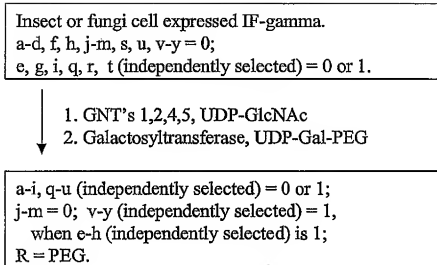


FIG. 35I

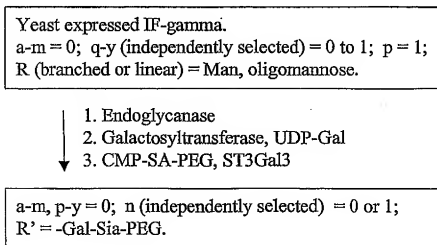


FIG. 35J

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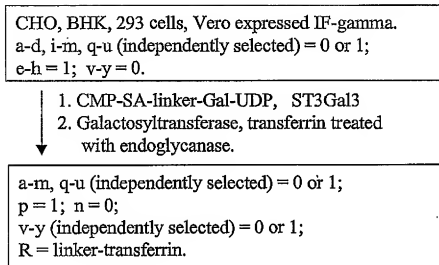


FIG. 35K

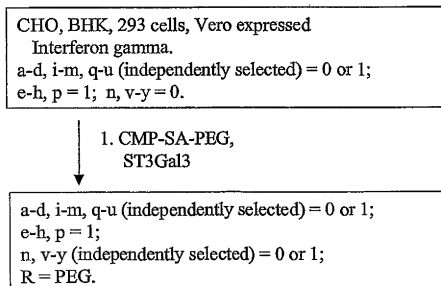


FIG. 35L

128/345

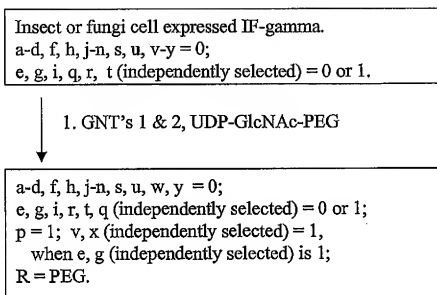


FIG. 35M

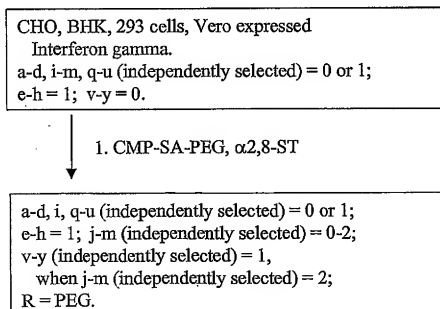
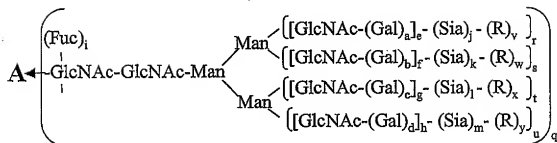
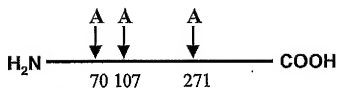


FIG. 35N

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a-d, i, q-u (independently selected) = 0 or 1.

e-h (independently selected) = 0 to 6.

j-m (independently selected) = 0 to 100.

v-y = 0; R = polymer.

FIG. 36A

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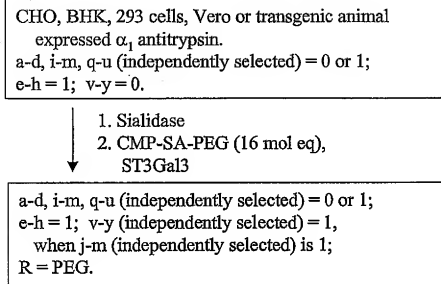


FIG. 36B

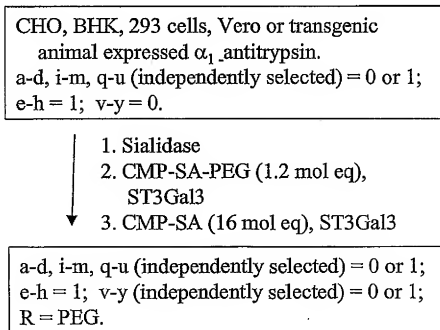


FIG. 36C

131/345

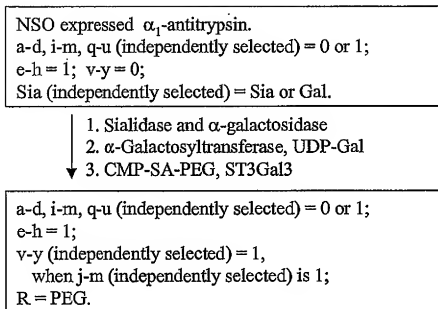


FIG. 36D

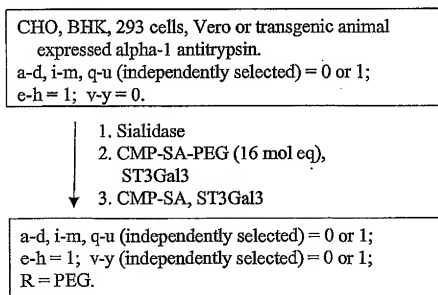


FIG. 36E

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CHO, BHK, 293 cells, Vero or transgenic animal
expressed α_1 -antitrypsin.
a-d, i-m, q-u (independently selected) = 0 or 1;
e-h = 1; v-y = 0.

- ↓
1. CMP-SA-levulinate, ST3Gal3,
buffer, salt
 2. H_4N_2 -PEG

a-d, i-m, q-u (independently selected) = 0 or 1;
e-h = 1; v-y (independently selected) = 0 or 1;
R = PEG.

FIG. 36F

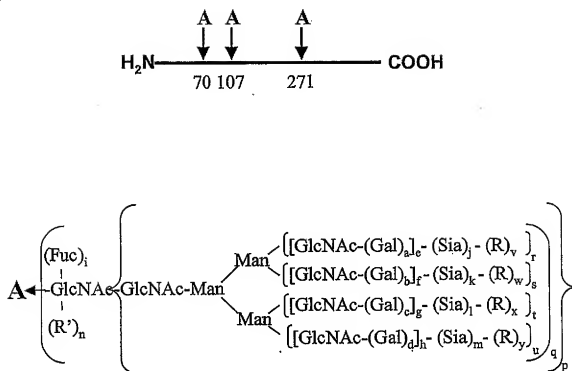
CHO, BHK, 293 cells, Vero expressed α_1 -antitrypsin.
a-d, i-m, q-u (independently selected) = 0 or 1;
e-h = 1; v-y = 0.

- ↓
1. CMP-SA, $\alpha 2,8$ -ST

a-d, i, q-u (independently selected) = 0 or 1; e-h = 1;
j-m (independently selected) = 0-20;
v-y (independently selected) = 0.

FIG. 36G

133/345



a-d, i, n, p-u (independently selected) = 0 or 1.

e-h (independently selected) = 0 to 6.

j-m (independently selected) = 0 to 100.

v-y = 0;

R = modifying group, mannose, oligo-mannose;

R' = H, glycosyl residue, modifying group, glycoconjugate.

FIG. 36H

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Insect or fungi cell expressed α_1 -antitrypsin.
 a-d, f, h, j-m, s, u, v-y = 0;
 e, g, i, q, r, t (independently selected) = 0 or 1.



1. GNT's 1,2,4,5, UDP-GlcNAc
2. Galactosyltransferase, UDP-Gal-PEG

a-i, q-u (independently selected) = 0 or 1; j-m = 0;
 v-y (independently selected) = 1,
 when e-h (independently selected) is 1;
 R = PEG.

FIG. 36I

Yeast expressed α_1 -antitrypsin.
 a-m = 0; q-y (independently selected) = 0 to 1;
 p = 1; R (branched or linear) = Man, oligomannose.



1. Endoglycanase
2. Galactosyltransferase, UDP-Gal
3. CMP-SA-PEG, ST3Gal3

a-m, p-y = 0; n (independently selected) = 0 or 1;
 R' = -Gal-Sia-PEG.

FIG. 36J

135/345

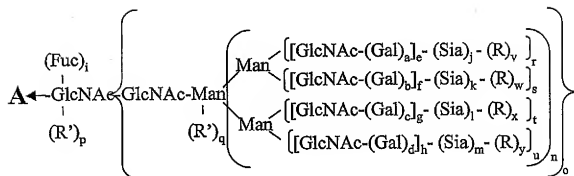
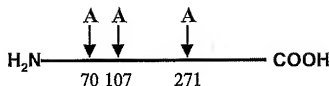
CHO, BHK, 293 cells, Vero expressed α_1 -antitrypsin.
a-d, i-m, q-u (independently selected) = 0 or 1;
e-h = 1; v-y = 0.

- ↓
1. CMP-SA-linker-Gal-UDP,
ST3Gal3
 2. Galactosyltransferase, transferrin treated
with endoglycanase

a-m, q-u (independently selected) = 0 or 1;
p = 1; n = 0;
v-y (independently selected) = 0 or 1;
R = linker-transferrin.

FIG. 36K

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a-d, i, n-u (independently selected) = 0 or 1.

e-h (independently selected) = 0 to 4.

j-m (independently selected) = 0 to 20.

R = polymer;

R', R'' (independently selected) = sugar, glycoconjugate.

FIG. 36L

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Yeast expressed alpha-1 antitrypsin.

a-h, i-m, p, q = 0;

R (independently selected) = mannose, oligomannose, polymannose;

r-u, v-y (independently selected) = 0 or 1; n, o = 1.

- ↓ 1. endoglycanase
 ↓ 2. Galactosyltransferase, UDP-Gal-PEG

a-h, i-o, q, r-u, v-y = 0; p = 1.

R'' = Gal-PEG.

FIG. 36M

Plant expressed alpha-1 antitrypsin.

a-d, f, h, j-m, s, u, v-y = 0;

e, g, i, q, r, t (independently selected) = 0 or 1;

n = 1; R' = xylose

- ↓ 1. hexosaminidase,
 2. alpha mannosidase and xylosidase
 ↓ 3. GlcNAc transferase, UDP-GlcNAc-PEG

a-d, f, h, j-n, s, u, v-y = 0;

e, g, i, r, t (independently selected) = 0;

q = 1; R' = GlcNAc-PEG.

FIG. 36N

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CHO, BHK, 293 cells, Vero, transgenic animal
expressed α_1 antitrypsin.
a-h, i-o, r-u (independently selected) = 0 or 1;
p, q, v-y = 0.



1. CMP-SA-PEG,
ST3Gal3

a-h, i-o, r-u (independently selected) = 0 or 1;
p, q = 0; v-y (independently selected) = 0 or 1;
R = PEG.

FIG. 360

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CHO, BHK, 293 cells, Vero expressed Cerezyme
a-d, i-m, q-u (independently selected) = 0 or 1;
e-h = 1; v-y = 0.

- ↓
1. Sialidase
 2. CMP-SA-PEG (16 mol eq),
ST3Gal3

a-d, i-m, q-u (independently selected) = 0 or 1;
e-h = 1; v-y (independently selected) = 1,
when j-m (independently selected) is 1;
R = PEG.

FIG. 37B

CHO, BHK, 293 cells, Vero expressed Cerezyme.
a-d, i-m, q-u (independently selected) = 0 or 1;
e-h = 1; v-y = 0.

- ↓
1. Sialidase
 2. CMP-SA-M-6-P (1.2 mol eq),
ST3Gal3
 3. CMP-SA (16 mol eq), ST3Gal3

a-d, i-m, q-u (independently selected) = 0 or 1;
e-h = 1; v-y (independently selected) = 0 or 1;
R = mannose-6-phosphate

FIG. 37C

141/345

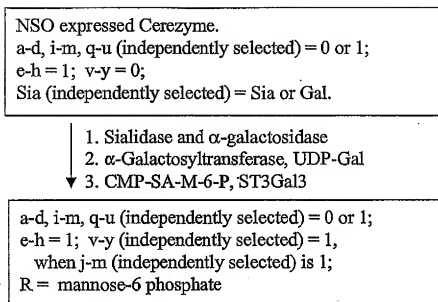


FIG. 37D

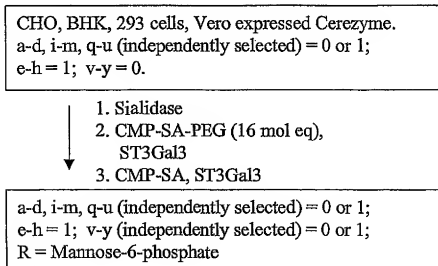


FIG. 37E

142/345

CHO, BHK, 293 cells, Vero expressed Cerezyme.
a-d, i-m, q-u (independently selected) = 0 or 1;
e-h = 1; v-y = 0.

- ↓
1. CMP-SA-levulinate, ST3Gal3,
buffer, salt.
 2. H₄N₂-spacer-M-6-P or clustered M-6-P

a-d, i-m, q-u (independently selected) = 0 or 1;
e-h = 1; v-y (independently selected) = 0 or 1;
R = M-6-P or clustered M-6-P

FIG. 37F

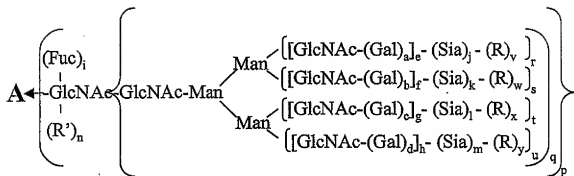
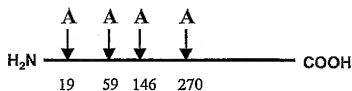
CHO, BHK, 293 cells, Vero expressed Cerezyme.
a-d, i-m, q-u (independently selected) = 0 or 1;
e-h = 1; v-y = 0.

- ↓
1. CMP-SA, α 2,8-ST

a-d, i, q-u (independently selected) = 0 or 1;
e-h = 1; j-m (independently selected) = 0-20;
v-y (independently selected) = 0.

FIG. 37G

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a-d, i, n, p-u (independently selected) = 0 or 1.

e-h (independently selected) = 0 to 6.

j-m (independently selected) = 0 to 100.

v-y = 0;

R = modifying group, mannose, oligo-mannose;

R' = H, glycosyl residue, modifying group,
glycoconjugate.

FIG. 37H

144/345

Insect cell expressed Cerezyme.

a-d, f, h, j-m, s, u, v-y = 0;

e, g, i, q, r, t (independently selected) = 0 or 1.



1. GNT's 1,2,4,5, UDP-GlcNAc

2. Galactosyltransferase, UDP-Gal-PEG

a-i, q-u (independently selected) = 0 or 1;

j-m = 0;

v-y (independently selected) = 1,

when e-h (independently selected) is 1;

R = PEG.

FIG. 37I

Yeast expressed Cerezyme.

a-m = 0; q-y (independently selected) = 0 to 1;

p = 1; R (branched or linear) = Man, oligomannose.



1. Endoglycanase

2. Galactosyltransferase, UDP-Gal

3. CMP-SA-PEG, ST3Gal3

a-m, p-y = 0; n (independently selected) = 0 or 1;

R' = -Gal-Sia-PEG.

FIG. 37J

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CHO, BHK, 293 cells, Vero expressed Cerezyme.
a-d, i-m, q-u (independently selected) = 0 or 1;
e-h = 1; v-y = 0.

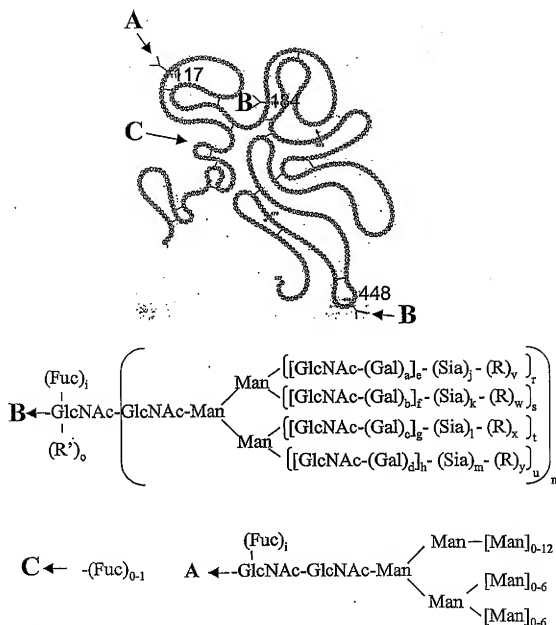


1. CMP-SA-linker-SA-CMP,
ST3Gal3
2. ST3Gal3, desialylated transferrin.
3. CMP-SA, ST3Gal3

a-m, q-u (independently selected) = 0 or 1;
p = 1; n = 0; v-y (independently selected) = 0 or 1;
R = linker-transferrin.

FIG. 37K

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a-d, i, n-u (independently selected) = 0 or 1.

e-h (independently selected) = 0 to 4.

j-m (independently selected) = 0 to 20.

R = polymer; R' = sugar, glycoconjugate.

FIG. 38A

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CHO, BHK, 293 cells, Vero expressed tPA
 a-g, n = 1; h = 1 to 3;
 j-m, i, (independently selected) = 0 or 1;
 r-u (independently selected) = 0 to 1; o, v-y = 0.

1. Mannosidase(s), sialidase
2. GNT1,2 (4 and/or 5) UDP-GlcNAc
3. Gal transferase, UDP-Gal
4. CMP-SA-PEG, ST3Gal3

A = B; a-g, n = 1; h = 1 to 3;
 i, r-u (independently selected) = 0 or 1;
 o = 0; j-m, v-y (independently selected) = 0 or 1;
 R = PEG

FIG. 38B

Insect or fungi cell expressed tPA
 A = B; a-d, f, h, j-o, s, u, v-y = 0;
 e, g, i, n, r, t (independently selected) = 0 or 1.

1. GNT's 1&2, UDP-GlcNAc
2. Galactosyltransferase, UDP-Gal
3. CMP-SA-PEG, ST3Gal3

A = B; b, d, f, h, k, m, o, s, u, w, y = 0;
 a, c, e, g, i, r, t (independently selected) = 0 or 1;
 n = 1; j, l, v, x (independently selected) = 0 or 1;
 R = PEG.

FIG. 38C

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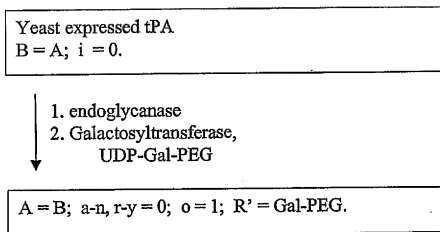


FIG. 38D

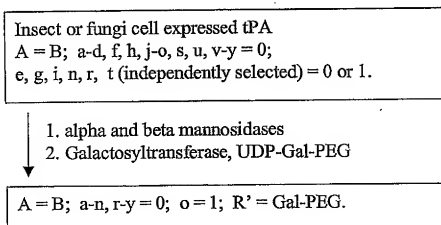


FIG. 38E

149/345

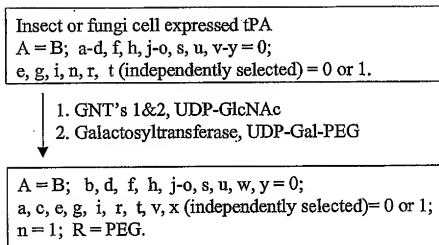


FIG. 38F

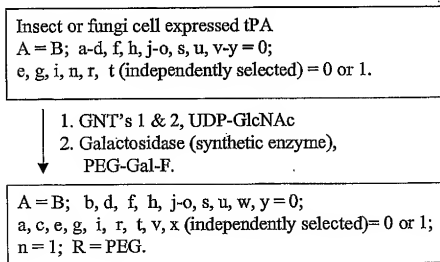


FIG. 38G

150/345

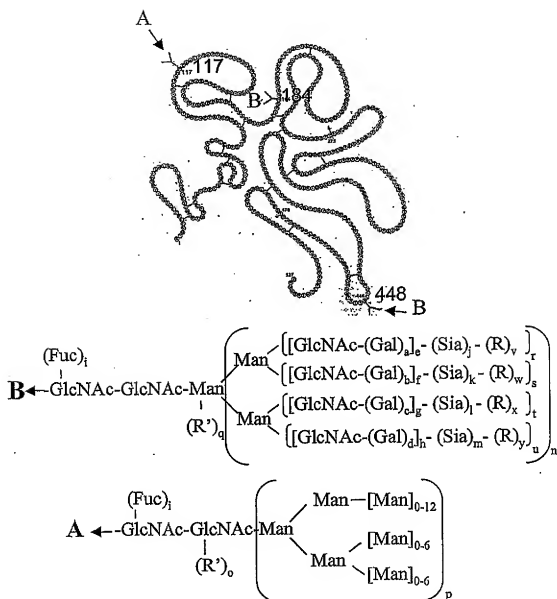


FIG. 38H

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NSO expressed tPA

A = B; a-m, r-u (independently selected) = 0 or 1;
 n = 1; o, p, q, v-y = 0

1. sialidase, alpha-galactosidase
2. CMP-SA-levulinate, ST3Gal3,
3. H₄N₂-PEG

A = B; a-m, r-y (independently selected) = 0 or 1;
 n = 1; o, p, q = 0;
 v-y (independently selected) = 1,
 when j-m (independently selected) is 1;
 R = PEG.

FIG. 38I

CHO, BHK, 293 cells, Vero expressed tPA

a-g, n, p = 1; h = 1 to 3;
 j-m, i, (independently selected) = 0 or 1;
 r-u (independently selected) = 0 to 1; q, o, v-y = 0.

1. alpha and beta Mannosidases
2. CMP-SA, ST3Gal3
3. Galactosyltransferase, UDP-Gal-PEG


a-g, n = 1; h = 1 to 3;
 i, r-u (independently selected) = 0 or 1; o = 1;
 q, p, v-y = 0; j-m (independently selected) = 0 or 1;
 R' = Gal-PEG

FIG. 38J

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Plant expressed tPA

A = B; a-d, f, h, j- m, s, u, v-y = 0;
e, g, i, q, r, t (independently selected) = 0 or 1;
n = 1; R' = xylose

- 
1. hexosaminidase,
 2. alpha mannosidase and
xylosidase
 3. GlcNAc transferase, UDP-
GlcNAc-PEG

A = B; a-d, f, h, j-n, s, u, v-y = 0;
e, g, i, r, t (independently selected) = 0;
q = 1; R' = GlcNAc-PEG.

FIG. 38K

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CHO, BHK, 293 cells, Vero expressed TNK tPA
a-d, i-m, q-u (independently selected) = 0 or 1;
e-h = 1; v-y = 0.



1. Sialidase
2. CMP-SA-PEG (16 mol eq),
ST3Gal3

a-d, i-m, q-u (independently selected) = 0 or 1;
e-h = 1; v-y (independently selected) = 1,
when j-m (independently selected) is 1;
R = PEG.

FIG. 38M

CHO, BHK, 293 cells, Vero expressed TNK tPA
a-d, i-m, q-u (independently selected) = 0 or 1;
e-h = 1; v-y = 0.



1. Sialidase
2. CMP-SA-PEG (1.2 mol eq),
ST3Gal3
3. CMP-SA (16 mol eq), ST3Gal3

a-d, i-m, q-u (independently selected) = 0 or 1;
e-h = 1; v-y (independently selected) = 0 or 1;
R = PEG.

FIG. 38N

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NSO expressed TNK tPA

a-d, i-m, q-u (independently selected) = 0 or 1;

e-h = 1; v-y = 0;

Sia (independently selected) = Sia or Gal.

- ↓
1. Sialidase and α -galactosidase
 2. Galactosyltransferase, UDP-Gal
 - ▼ 3. CMP-SA-PEG, ST3Gal3

a-d, i-m, q-u (independently selected) = 0 or 1;

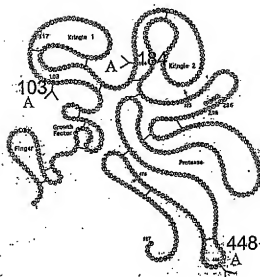
e-h = 1; v-y (independently selected) = 1,

when j-m (independently selected) is 1;

R = PEG.

FIG. 380

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CHO, BHK, 293 cells, Vero expressed TNK tPA
a-d, i-m, q-u (independently selected) = 0 or 1;
e-h = 1; v-y = 0.

- ↓
1. Sialidase
 2. CMP-SA-PEG (16 mol eq),
ST3Gal3
 3. CMP-SA, ST3Gal3

a-d, i-m, q-u (independently selected) = 0 or 1;
e-h = 1; v-y (independently selected) = 0 or 1;
R = PEG.

FIG. 38Q

CHO, BHK, 293 cells, Vero expressed TNK tPA
a-d, i-m, q-u (independently selected) = 0 or 1;
e-h = 1; v-y = 0.

- ↓
1. CMP-SA-levulinate, ST3Gal3,
buffer, salt
 2. H_4N_2 -PEG

a-d, i-m, q-u (independently selected) = 0 or 1;
e-h = 1; v-y (independently selected) = 0 or 1;
R = PEG.

FIG. 38R

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CHO, BHK, 293 cells, Vero expressed TNK tPA
a-d, i-m, q-u (independently selected) = 0 or 1;
e-h = 1; v-y = 0.



1. CMP-SA, α 2,8-ST

a-d, i, q-u (independently selected) = 0 or 1;
e-h = 1; j-m (independently selected) = 0-20;
v-y (independently selected) = 0.

FIG. 38S

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Insect cell expressed TNK tPA

a-d, f, h, j-m, s, u, v-y = 0;

e, g, i, q, r, t (independently selected) = 0 or 1.



1. GNT's 1,2,4,5, UDP-GlcNAc

2. Galactosyltransferase, UDP-Gal-PEG

a-i, q-u (independently selected) = 0 or 1;

j-m = 0; v-y (independently selected) = 1,

when e-h (independently selected) is 1;

R = PEG.

FIG. 38U

Yeast expressed TNK tPA

a-m = 0; q-y (independently selected) = 0 to 1; p = 1;

R (branched or linear) = Man, oligomannose.



1. Endoglycanase

2. Galactosyltransferase, UDP-Gal-PEG

a-m, p-y = 0; n (independently selected) = 0 or 1;

R' = -Gal-PEG.

FIG. 38V

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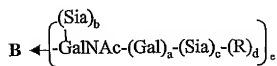
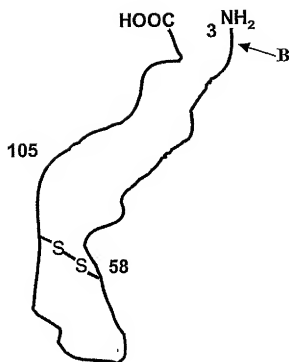
CHO, BHK, 293 cells, Vero expressed TNK tPA
a-d, i-m, q-u (independently selected) = 0 or 1;
e-h = 1; v-y = 0.

- ↓
1. CMP-SA-linker-Gal-UDP,
ST3Gal3
 2. Galactosyltransferase, anti-TNF
IG chimera produced in CHO.

a-m, r-u (independently selected) = 0 or 1; p, q = 1;
n = 0; v-y (independently selected) = 0 or 1;
R = linker-anti-TNF IG chimera protein.

FIG. 38W

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a-c, e (independently selected) = 0 or 1;
 d = 0;
 R = modifying group, mannose, oligo-
 mannose.

FIG. 39A

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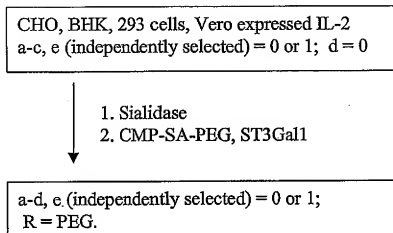


FIG. 39B

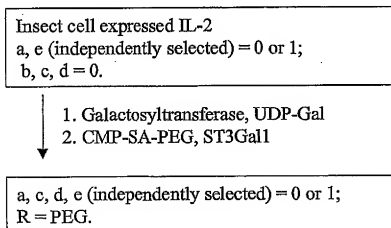


FIG. 39C

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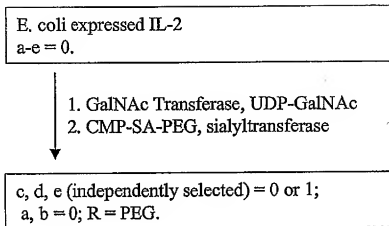


FIG. 39D

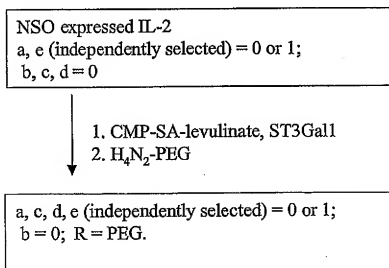


FIG. 39E

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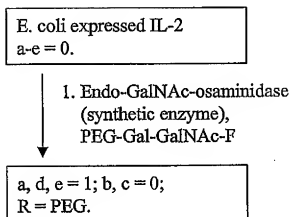


FIG. 39F

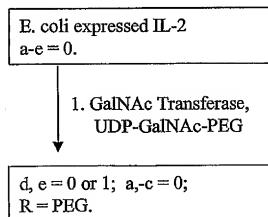
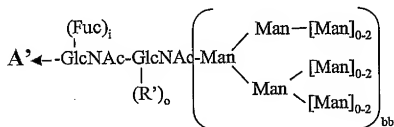
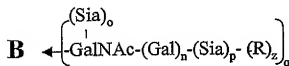
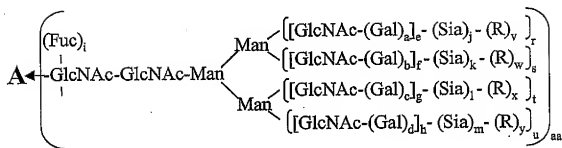


FIG. 39G

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2 peptides
A and A' - N-linked sites
B - O-linked sites



Alternate structure
for some N-linked
structures of A.

a-d, i, n-u (independently selected) = 0 or 1.

aa, bb (independently selected) = 0 or 1.

e-h (independently selected) = 0 to 6.

j-m (independently selected) = 0 to 20.

v-z = 0; R = polymer, glycoconjugate.

FIG. 40A

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CHO, BHK, 293s cells, Vero, MDCK, HEKC expressed
Factor VIII.

e-h = 1 to 4;

aa, bb, a-d, j-m, i, n-u (independently selected) = 0 or 1;

v-z = 0.



1. Sialidase

2. CMP-SA-PEG, ST3Gal3

e-h = 1 to 4;

aa, bb, a-d, i, n, q-u (independently selected) = 0 or 1;

o, p, z = 0; j-m, v-y (independently selected) = 0 or 1;

R = PEG.

FIG. 40B

CHO, BHK, 293S cells, Vero, MDCK, 293S, HEKC
expressed Factor VIII.

e-h = 1 to 4;

aa, bb, a-d, j-m, i, n-u (independently selected) = 0 or 1;

v-z = 0.



1. Sialidase

2. CMP-SA-PEG, ST3Gal3

3. ST3Gal1, CMP-SA

e-h = 1 to 4;

aa, bb, a-d, i, n, p-u (independently selected) = 0 or 1;

o, z = 0; j-m, v-y (independently selected) = 0 or 1;

R = PEG.

FIG. 40C

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CHO, BHK, 293s cells, Vero, MDCK, HEKC
expressed Factor VIII.
e-h = 1 to 4;
aa, bb, a-d, j-m, i, n-u (independently selected)=0 or 1;
v-z = 0.

↓
1. CMP-SA-PEG, ST3Gal3

e-h = 1 to 4;
aa, bb, a-d, i, n-u (independently selected) = 0 or 1;
z = 0; j-m, v-y (independently selected) = 0 or 1;
R = PEG.

FIG. 40D

CHO, BHK, 293S cells, Vero, MDCK, HEKC
expressed Factor VIII.
e-h = 1 to 4;
aa, bb, a-d, j-m, i, n-u (independently selected) 0 or 1;
v-z = 0.

↓
1. CMP-SA-PEG, ST3Gal1

e-h = 1 to 4;
aa, bb, a-d, i, n-u (independently selected) = 0 or 1;
z = 0; j-m, v-y (independently selected) = 0 or 1;
R = PEG.

FIG. 40E

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CHO, BHK, 293S cells, Vero, MDCK, HEKC
expressed Factor VIII.

e-h = 1 to 4;

aa, bb, a-d, j-m, i, n-u (independently selected)=0 or 1;

v-z = 0.



1. CMP-SA-PEG, α 2,8-ST

e-h = 1 to 4;

aa, bb, a-d, i, n-y (independently selected) = 0 or 1;

z = 0; j-m (independently selected) = 0 to 2;

v-y (independently selected) = 1,

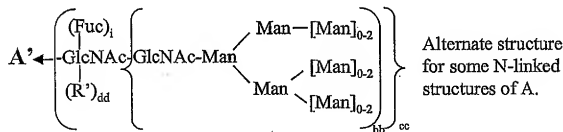
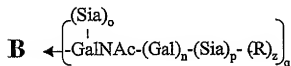
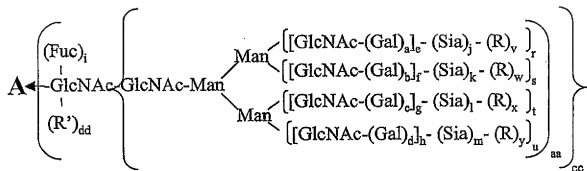
when j-m (independently selected) is 2;

R = PEG.

FIG. 40F

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2 peptides

A or A' - N-linked sites**B** - O-linked sites

a-d, i, n-u, (independently selected) = 0 or 1.

aa, bb, cc, dd (independently selected) = 0 or 1.

e-h (independently selected) = 0 to 6.

j-m (independently selected) = 0 to 20.

v-z = 0;

R = modifying group, mannose, oligo-mannose.

R' = H, glycosyl residue, modifying group, glycoconjugate.

FIG. 40G

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CHO, BHK, 293S cells, Vero, MDCK, HEKC
expressed Factor VIII.

e-h = 1 to 4;

aa, bb, cc, a-d, j-m, i, n-u (independently selected) = 0 or 1;

dd, v-z = 0.

- ↓
1. CMP-SA-levulinate, ST3Gal3,
2. H_4N_2 -PEG

e-h = 1 to 4;

aa, bb, cc, a-d, i, n-u (independently selected) = 0 or 1;

dd, z = 0; j-m, v-y (independently selected) = 0 or 1;

R = PEG.

FIG. 40H

CHO, BHK, 293S cells, Vero, MDCK, HEKC
expressed Factor VIII.

e-h = 1 to 4;

aa, bb, cc, a-d, j-m, i, n-u (independently selected) = 0 or 1;

dd, v-z = 0.

- ↓
1. endo-H
2. galactosyltransferase, UDP-Gal-PEG

e-h = 1 to 4;

aa, bb, dd, a-d, i, j-u (independently selected) = 0 or 1;

cc, v-z = 0; R' = -Gal-PEG.

FIG. 40I

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CHO, BHK, 293S cells, Vero, MDCK, HEKC
expressed Factor VIII.

e-h = 1 to 4;

aa, bb, cc, a-d, j-m, i, n-u (independently selected) = 0 or 1;

dd, v-z = 0.

- ↓
1. ST3Gal3, CMP-SA
 2. endo-H
 3. galactosyltransferase, UDP-Gal-PEG

e-h = 1 to 4;

aa, bb, dd, a-d, i, j-u (independently selected) = 0 or 1;

cc, v-z = 0; R' = -Gal-PEG.

FIG. 40J

CHO, BHK, 293S cells, Vero, MDCK, HEKC
expressed Factor VIII.

e-h = 1 to 4;

aa, bb, cc, a-d, j-m, i, n-u (independently selected) = 0 or 1;

dd, v-z = 0.

- ↓
1. mannosidases
 2. GNT 1 & 2, UDP-GlcNAc
 3. galactosyltransferase, UDP-Gal-PEG

e-h = 1 to 4;

aa, a-d, i, j-y (independently selected) = 0 or 1;

bb, cc, dd, z = 0; R = PEG.

FIG. 40K

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CHO, BHK, 293S cells, Vero, MDCK, HEKC
expressed Factor VIII.

e-h = 1 to 4;

aa, bb, cc, a-d, j-m, i, n-u (independently selected) = 0 or 1;

dd, v-z = 0.

- ↓
1. mannosidases
 2. GNT-1, 2, 4 & 5; UDP-GlcNAc
 3. galactosyltransferase, UDP-Gal
 4. ST3Gal3, CMP-SA

e-h = 1 to 4;

aa, bb, cc, a-d, i, j-q (independently selected) = 0 or 1;

dd, v-z = 0.

FIG. 40L

CHO, BHK, 293S cells, Vero, MDCK, HEKC
expressed Factor VIII.

e-h = 1 to 4;

aa, bb, cc, a-d, j-m, i, n-u (independently selected) = 0 or 1;

dd, v-z = 0.

- ↓
1. mannosidases
 2. GNT-1, UDP-GlcNAc-PEG

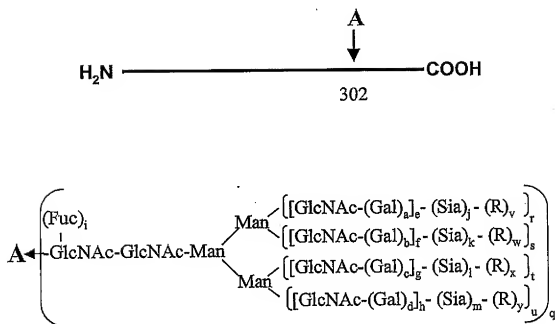
e-h = 0 to 4;

aa, a-d, i, j-y (independently selected) = 0 or 1;

bb, cc, dd, z = 0.

FIG. 40M

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a-d, i, q-u (independently selected) = 0 or 1.
 e-h (independently selected) = 0 to 6.
 j-m (independently selected) = 0 to 100.
 v-y = 0; R = polymer.

FIG. 41A

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CHO, BHK, 293 cells, Vero expressed Urokinase.
a-d, i-m, q-u (independently selected) = 0 or 1;
e-h = 1; v-y = 0.

- ↓
1. Sialidase
 2. CMP-SA-PEG (16 mol eq),
ST3Gal3

a-d, i-m, q-u (independently selected) = 0 or 1;
e-h = 1; v-y (independently selected) = 1,
when j-m (independently selected) is 1;
R = PEG.

FIG. 41B

CHO, BHK, 293 cells, Vero expressed Urokinase.
a-d, i-m, q-u (independently selected) = 0 or 1;
e-h = 1; v-y = 0.

- ↓
1. Sialidase
 2. CMP-SA-PEG (1.2 mol eq),
ST3Gal3
 3. CMP-SA (16 mol eq), ST3Gal3

a-d, i-m, q-u (independently selected) = 0 or 1;
e-h = 1; v-y (independently selected) = 0 or 1;
R = PEG.

FIG. 41C

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NSO expressed Urokinase.

a-d, i-m, q-u (independently selected) = 0 or 1;

e-h = 1; v-y = 0;

Sia (independently selected) = Sia or Gal.

- ↓
1. Sialidase and α -galactosidase
 2. α -Galactosyltransferase, UDP-Gal
 3. CMP-SA-PEG, ST3Gal3

a-d, i-m, q-u (independently selected) = 0 or 1;

e-h = 1; v-y (independently selected) = 1,

when j-m (independently selected) is 1;

R = PEG.

FIG. 41D

CHO, BHK, 293 cells, Vero expressed Urokinase.

a-d, i-m, q-u (independently selected) = 0 or 1;

e-h = 1; v-y = 0.

- ↓
1. Sialidase
 2. CMP-SA-PEG (16 mol eq),
ST3Gal3
 3. CMP-SA, ST3Gal3

a-d, i-m, q-u (independently selected) = 0 or 1;

e-h = 1; v-y (independently selected) = 0 or 1;

R = PEG.

FIG. 41E

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CHO, BHK, 293 cells, Vero expressed Urokinase.
a-d, i-m, q-u (independently selected) = 0 or 1;
e-h = 1; v-y = 0.

- ↓
1. CMP-SA-levulinate, ST3Gal3,
buffer, salt
 2. H_4N_2 -PEG

a-d, i-m, q-u (independently selected) = 0 or 1;
e-h = 1; v-y (independently selected) = 0 or 1;
R = PEG.

FIG. 41F

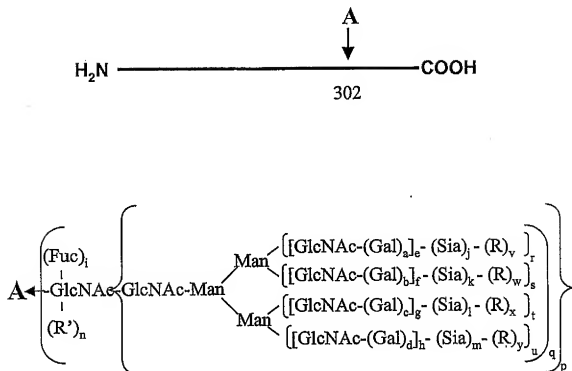
CHO, BHK, 293 cells, Vero expressed Urokinase.
a-d, i-m, q-u (independently selected) = 0 or 1;
e-h = 1; v-y = 0.

- ↓
1. CMP-SA, $\alpha 2,8$ -ST

a-d, i, q-u (independently selected) = 0 or 1;
e-h = 1;
j-m (independently selected) = 0-20;
v-y (independently selected) = 0.

FIG. 41G

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a-d, i, n, p-u (independently selected) = 0 or 1.

e-h (independently selected) = 0 to 6.

j-m (independently selected) = 0 to 100.

v-y = 0;

R = modifying group, mannose, oligo-mannose;

R' = H, glycosyl residue, modifying group,
glycoconjugate.

FIG. 41H

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Insect cell expressed Urokinase.

a-d, f, h, j-n, s, u, v-y = 0;

e, g, i, q, r, t (independently selected) = 0 or 1.



1. GNT's 1,2,4,5, UDP-GlcNAc

2. Galactosyltransferase, UDP-Gal-PEG

a-i, q-u (independently selected) = 0 or 1;

j-n = 0; v-y (independently selected) = 1,

when e-h (independently selected) is 1;

R = PEG.

FIG. 41I

Yeast expressed Urokinase.

a-n = 0;

q-y (independently selected) = 0 to 1;

p = 1; R (branched or linear) = Man, oligomannose.



1. Endoglycanase

2. Galactosyltransferase, UDP-Gal

3. CMP-SA-PEG, ST3Gal3

a-m, p-y = 0; n (independently selected) = 0 or 1;

R' = -Gal-Sia-PEG.

FIG. 41J

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CHO, BHK, 293 cells, Vero expressed Urokinase.

a-d, i-m, q-u (independently selected) = 0 or 1;

e-h = 1; n, v-y = 0.

↓ 1. CMP-SA-linker-SA-CMP, ST3Gal3

2. ST3Gal1, desialylated Urokinase produced in CHO.

↓ 3. CMP-SA, ST3Gal3, ST3Gal1

a-m, q-u (independently selected) = 0 or 1;

p = 1; n = 0;

v-y (independently selected) = 0 or 1;

R = linker-Urokinase.

FIG. 41K

Isolated Urokinase.

a-d, i-m, q-u (independently selected) = 0 or 1;

e-h = 1; v-y = 0; n = 0;

Sia (independently selected) = Sia or SO₄;

Gal (independently selected) = Gal or GalNAc;

GlcNAc (independently selected) = GlcNAc or GlcNAc-Fuc.

↓ 1. sulfohydrolase

2. CMP-SA-PEG, sialyltransferase

a-d, i-m, q-u (independently selected) = 0 or 1;

n = 0; e-h = 1; Sia = Sia;

Gal (independently selected) = Gal or GalNAc;

GlcNAc (independently selected) = GlcNAc or GlcNAc-Fuc.

v-y (independently selected) = 0 or 1;

R = PEG.

FIG. 41L

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Isolated Urokinase.

a-d, i-m, q-u (independently selected) = 0 or 1;

e-h = 1; n = 0; v-y = 0;

Sia (independently selected) = Sia or SO₄;

Gal (independently selected) = Gal or GalNAc;

GlcNAc (independently selected) = GlcNAc or GlcNAc-Fuc.



1. sulfohydrolase, hexosaminidase

2. UDP-Gal-PEG, galactosyltransferase

a-d, i, q-u (independently selected) = 0 or 1;

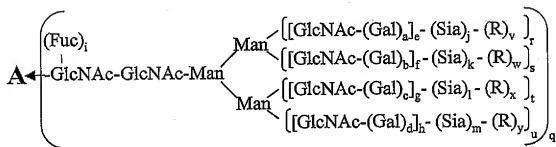
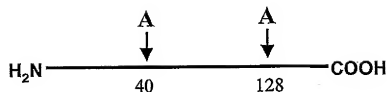
e-h = 1; j-n = 0; Gal (independently selected) = Gal;

GlcNAc (independently selected) = GlcNAc or GlcNAc-Fuc;

v-y (independently selected) = 0 or 1; R = PEG.

FIG. 41M

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a-d, i, q-u (independently selected) = 0 or 1.

e-h (independently selected) = 0 to 6.

j-m (independently selected) = 0 to 100.

v-y = 0; R = polymer, glycoconjugate.

FIG. 42A

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CHO, BHK, 293 cells, Vero expressed DNase I.
a-d, i-m, q-u (independently selected) = 0 or 1;
e-h = 1; v-y = 0.



1. Sialidase
2. CMP-SA-PEG (16 mol eq),
ST3Gal3

a-d, i-m, q-u (independently selected) = 0 or 1;
e-h = 1;
v-y (independently selected) = 1,
when j-m (independently selected) is 1;
R = PEG.

FIG. 42B

CHO, BHK, 293 cells, Vero expressed DNase I.
a-d, i-m, q-u (independently selected) = 0 or 1;
e-h = 1; v-y = 0.



1. Sialidase
2. CMP-SA-PEG (1.2 mol eq), ST3Gal3
3. CMP-SA (16 mol eq), ST3Gal3

a-d, i-m, q-u (independently selected) = 0 or 1;
e-h = 1; v-y (independently selected) = 0 or 1;
R = PEG.

FIG. 42C

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NSO expressed DNase I.

a-d, i-m, q-u (independently selected) = 0 or 1;

e-h = 1; v-y = 0;

Sia (independently selected) = Sia or Gal.

- ↓
1. Sialidase and α -galactosidase
 2. α -Galactosyltransferase, UDP-Gal
 3. CMP-SA-PEG, ST3Gal3

a-d, i-m, q-u (independently selected) = 0 or 1;

e-h = 1; v-y (independently selected) = 1,

when j-m (independently selected) is 1;

R = PEG.

FIG. 42D

CHO, BHK, 293 cells, Vero expressed DNase I.

a-d, i-m, q-u (independently selected) = 0 or 1;

e-h = 1; v-y = 0.

- ↓
1. Sialidase
 2. CMP-SA-PEG (16 mol eq), ST3Gal3
 3. CMP-SA, ST3Gal3

a-d, i-m, q-u (independently selected) = 0 or 1;

e-h = 1; v-y (independently selected) = 0 or 1;

R = PEG.

FIG. 42E

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CHO, BHK, 293 cells, Vero expressed DNase I.
a-d, i-m, q-u (independently selected) = 0 or 1;
e-h = 1; v-y = 0.

- ↓
1. CMP-SA-levulinate, ST3Gal3,
buffer, salt
 2. H_4N_2 -PEG

a-d, i-m, q-u (independently selected) = 0 or 1;
e-h = 1; v-y (independently selected) = 0 or 1;
R = PEG.

FIG. 42F

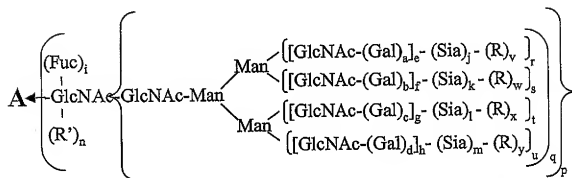
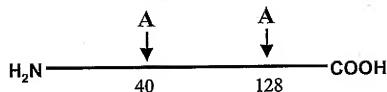
CHO, BHK, 293 cells, Vero expressed DNase I.
a-d, i-m, q-u (independently selected) = 0 or 1;
e-h = 1; v-y = 0.

- ↓
1. CMP-SA, $\alpha 2,8$ -ST

a-d, i, q-u (independently selected) = 0 or 1;
e-h = 1;
j-m (independently selected) = 0-20;
v-y (independently selected) = 0.

FIG. 42G

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a-d, i, n, p-u (independently selected) = 0 or 1.

e-h (independently selected) = 0 to 6.

j-m (independently selected) = 0 to 100.

v-y = 0;

R = modifying group, mannose, oligo-mannose;

R' = H, glycosyl residue, modifying group,

glycoconjugate.

FIG. 42H

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Insect cell expressed DNase I.

a-d, f, h, j-n, s, u, v-y = 0;

e, g, i, q, r, t (independently selected) = 0 or 1.



1. GNT's 1,2,4,5, UDP-GlcNAc

2. Galactosyltransferase, UDP-Gal-PEG

a-i, q-u (independently selected) = 0 or 1; j-n = 0;

v-y (independently selected) = 1,

when e-h (independently selected) is 1;

R = PEG.

FIG. 42I

Yeast expressed DNase I.

a-n = 0;

q-y (independently selected) = 0 to 1;

p = 1; R (branched or linear) = Man, oligomannose.



1. Endoglycanase

2. Galactosyltransferase, UDP-Gal

3. CMP-SA-PEG, ST3Gal3

a-n, p-y = 0; n (independently selected) = 0 or 1;

R' = -Gal-Sia-PEG.

FIG. 42J

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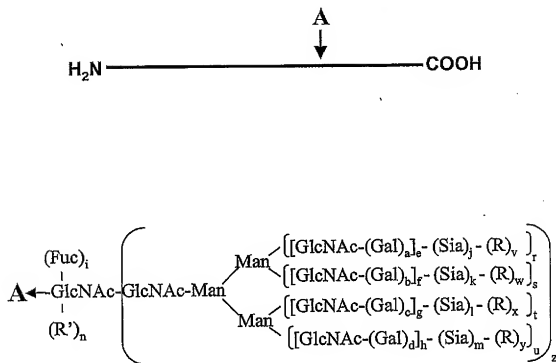
CHO, BHK, 293 cells, Vero expressed DNase I.
a-d, i-m, q-u (independently selected) = 0 or 1;
e-h = 1; n, v-y = 0.

- ↓
1. CMP-SA-linker-SA-CMP, ST3Gal3
 2. ST3Gal1, desialylated alpha-1-Proteinase inhibitor.
 3. CMP-SA, ST3Gal3, ST3Gal1

a-m, q-u (independently selected) = 0 or 1;
p = 1; n = 0;
v-y (independently selected) = 0 or 1;
R = linker- alpha-1-Proteinase inhibitor.

FIG. 42K

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a-d, i, r-u (independently selected) = 0 or 1.

e-h (independently selected) = 0 to 4.

j-m (independently selected) = 0 or 1.

n, v-y = 0; z = 0 or 1;

R = modifying group, mannose, oligo-mannose;

R' = H, glycosyl residue, modifying group,
glycoconjugate.

FIG. 43A

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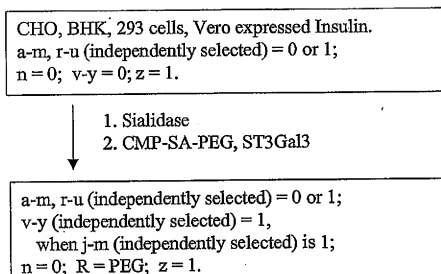


FIG. 43B

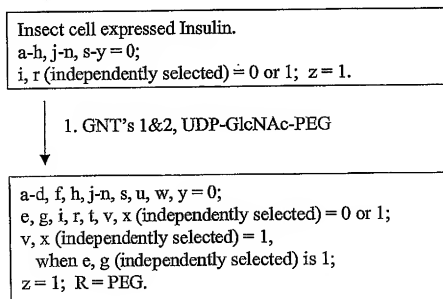


FIG. 43C

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Yeast expressed Insulin.

a-n = 0; r-y (independently selected) = 0 to 1;

z = 1;

R (branched or linear) = Man, oligomannose or
polysaccharide.



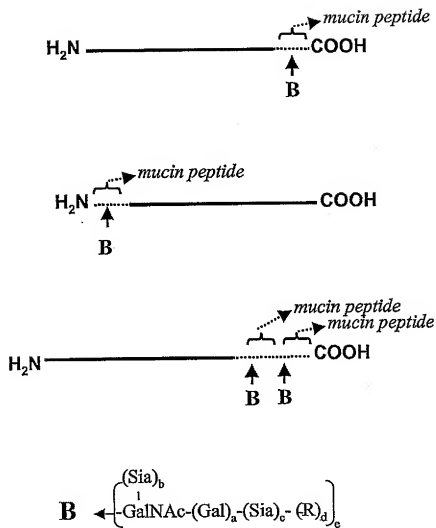
1. Endo-H

2. Galactosyltransferase, UDP-Gal-PEG

a-m, r-z= 0; n = 1; R' = -Gal-PEG.

FIG. 43D

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a-c, e (independently selected) = 0 or 1;
d = 0; R = polymer

FIG. 43E

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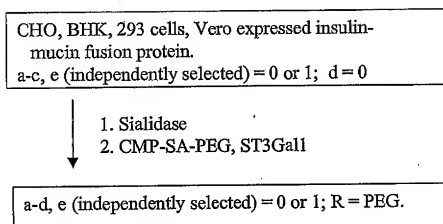


FIG. 43F

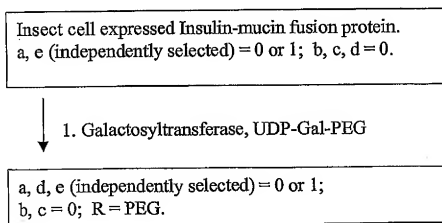


FIG. 43G

194/345

E. coli expressed Insulin-mucin fusion protein.
a-e = 0.

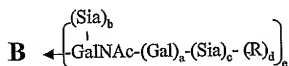
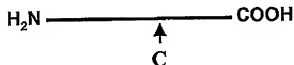
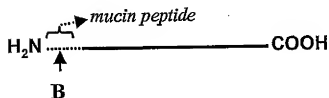
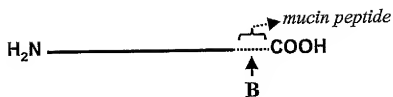


1. GalNAc Transferase, UDP-GalNAc
2. CMP-SA-PEG, sialyltransferase

c, d, e (independently selected) = 0 or 1;
a, b = 0; R = PEG.

FIG. 43H

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a-c, e (independently selected) = 0 or 1;
 d = 0; R = modifying group, mannose,
 oligo-mannose.

FIG. 43I

196/345

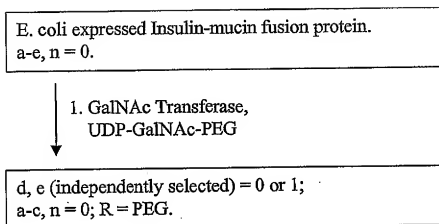


FIG. 43J

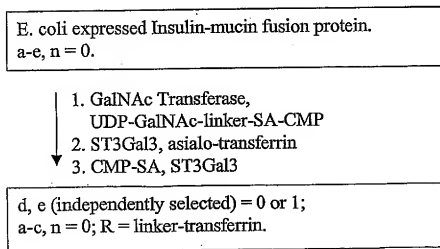


FIG. 43K

197/345

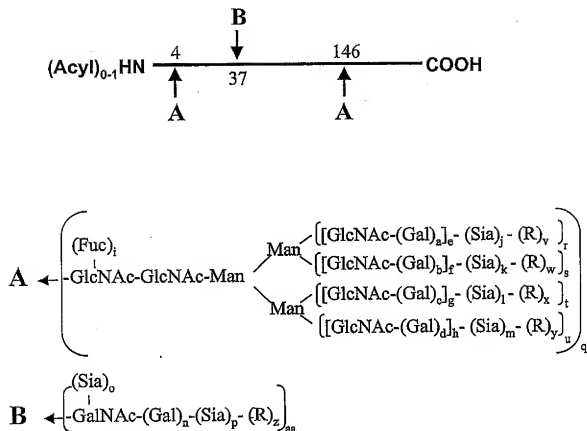
E. coli expressed Insulin (N)—no mucin peptide.
a-e, n = 0.

- ↓
1. NHS-CO-linker-SA-CMP
 2. ST3Gal3, asialo-transferrin
 3. CMP-SA, ST3Gal3

a-e = 0; n = 1;
R' = linker-transferrin.

FIG. 43L

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a-d, i, n-u, aa (independently selected) = 0 or 1.

e-h (independently selected) = 0 to 6.

j-m (independently selected) = 0 to 100.

v-y = 0; R = polymer, glycoconjugate.

FIG. 44A

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CHO, BHK, 293 cells, Vero expressed M-antigen.
a-d, i-m, o-u, aa (independently selected) = 0 or 1;
n, e-h = 1; v-z = 0.

- ↓
1. Sialidase
 2. CMP-SA-linker-lipid-A,
ST3Gal3

a-d, i-m, q-u, aa (independently selected) = 0 or 1;
o, p, z = 0; n, e-h = 1;
v-y (independently selected) = 1,
when j-m (independently selected) is 1;
R = linker-lipid-A.

FIG. 44B

CHO, BHK, 293 cells, Vero expressed M-antigen.
a-d, i-m, o-u, aa (independently selected) = 0 or 1;
n, e-h = 1; v-z = 0.

- ↓
1. sialidase
 2. CMP-SA-linker-tetanus toxin, ST3Gal1
 3. CMP-SA, ST3Gal3

a-d, i-m, p-u, z, aa (independently selected) = 0 or 1;
o, v-y = 0; n, e-h = 1; R = tetanus toxin.

FIG. 44C

200/345

NSO expressed M-antigen.

a-d, i-n, o-u, aa (independently selected) = 0 or 1;

e-h = 1; v-z = 0;

Sia (independently selected) = Sia or Gal.

- ↓
1. α -galactosidase
 2. CMP-SA, ST3Gal3
 2. CMP-SA-KLH, ST3Gal1

a-d, i-n, p-u, z, aa (independently selected) = 0 or 1;

e-h = 1; o, v-y = 0;

z = 1, when p = 1;

R = KLH.

FIG. 44D

Yeast expressed M-antigen.

a-p, z = 0; q-y, aa (independently selected) = 0 to 1;

R (branched or linear) = Man, oligomannose;

GalNAc = Man.

- ↓
1. α 1,2-mannosidase
 2. GNT 1,
- ↓ UDP-GlcNAc-linker-diphtheria toxin.

e, q, l, m, r, t, u, v, aa (independently selected) = 0 or 1;

a-d, f-h, j, k, n-p, s, w-z = 0;

Sia = Man; R = linker-diphtheria toxin.

FIG. 44E

201/345

CHO, BHK, 293 cells, Vero expressed M-antigen.
a-d, i-m, o-u, aa (independently selected) = 0 or 1;
n, e-h = 1; v-z = 0.

- ↓
1. CMP-SA-levulinate, ST3Gal3,
 2. H_4N_2 -linker-DNA

a-d, i-m, o-y, aa (independently selected) = 0 or 1;
z = 0; n, e-h = 1; R = linker-DNA.

FIG. 44F

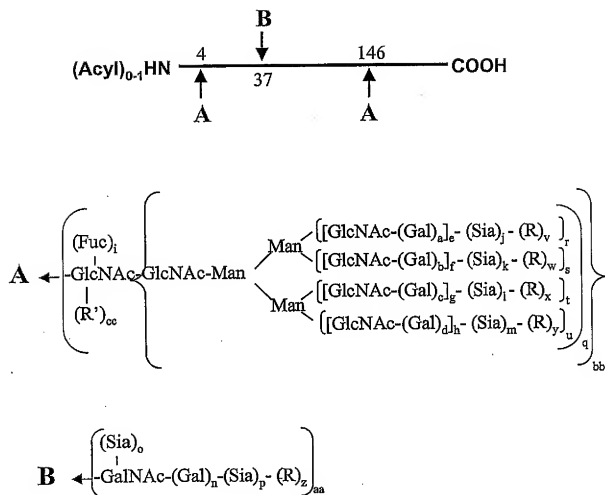
CHO, BHK, 293 cells, Vero expressed M-antigen.
a-d, i-n, o-u, aa (independently selected) = 0 or 1;
e-h = 1; v-z = 0.

- ↓
1. CMP-SA, poly- α 2,8-ST

a-d, i, n-u, aa (independently selected) = 0 or 1;
e-h = 1; j-m (independently selected) = 0-100;
v-z (independently selected) = 0.

FIG. 44G

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a-d, i, n, q-u, aa, bb, (independently selected) = 0 or 1.

e-h (independently selected) = 0 to 6.

j-p (independently selected) = 0 to 100.

Cc, v-y = 0;

R = modifying group, mannose, oligo-mannose.

R' = H, glycosyl residue, modifying group,
glycoconjugate.

FIG. 44H

203/345

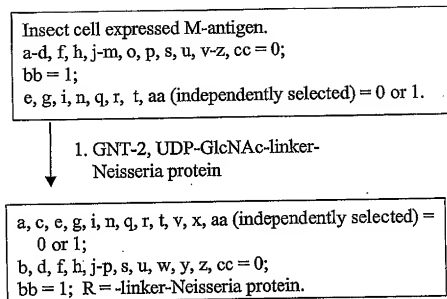


FIG. 44I

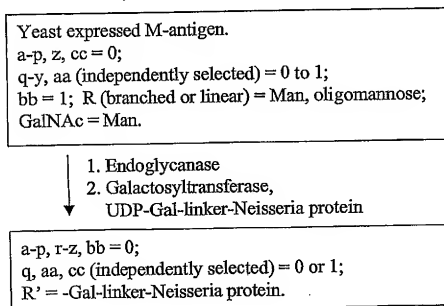


FIG. 44J

204/345

Yeast expressed M-antigen.

a-p, z, cc = 0;

q-y, aa (independently selected) = 0 to 1; bb = 1;

R (branched or linear) = Man, oligomannose;

GalNAc = Man.

1. mannosidases

2. GNT 1 & 2, UDP-GlcNAc

3. UDP-Gal, Galactosyltransferase,

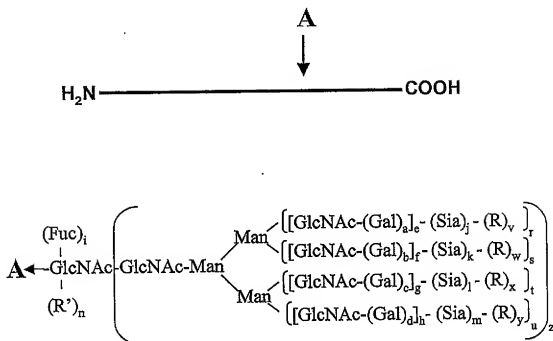
4. CMP-SA, sialyltransferase

a, c, e, g, j, l, q, r, t, aa (independently selected) = 0 or 1;

b, d, f, h, k, m-p, s, u-z, cc = 0; bb = 1.

FIG. 44K

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a-d, i, r-u (independently selected) = 0 or 1.

e-h (independently selected) = 0 to 4.

j-m (independently selected) = 0 or 1.

n, v-y = 0; z = 0 or 1;

R = modifying group, mannose, oligo-mannose;

R' = H, glycosyl residue, modifying group,

glycoconjugate.

FIG. 45A

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CHO, BHK, 293 cells, Vero expressed Growth Hormone.

a-m, r-u (independently selected) = 0 or 1;
n = 0; v-y = 0; z = 1.

1. Sialidase
2. CMP-SA-PEG, ST3Gal3

a-m, r-u (independently selected) = 0 or 1;
v-y (independently selected) = 1,
when j-m (independently selected) is 1;
n = 0; R = PEG; z = 1.

FIG. 45B

Insect cell expressed growth hormone.

a-h, j-n, s-y = 0;
i, r (independently selected) = 0 or 1; z = 1.

1. GNT's 1&2, UDP-GlcNAc-PEG

a-d, f, h, j-n, s, u, w, y = 0;
e, g, i, r, t, v, x (independently selected) = 0 or 1;
v, x (independently selected) = 1,
when e, g (independently selected) is 1;
z = 1; R = PEG.

FIG. 45C

207/345

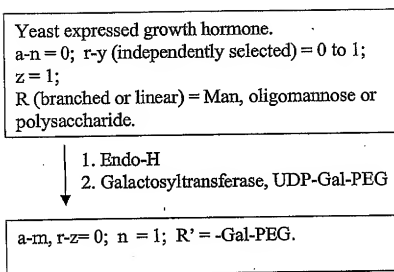
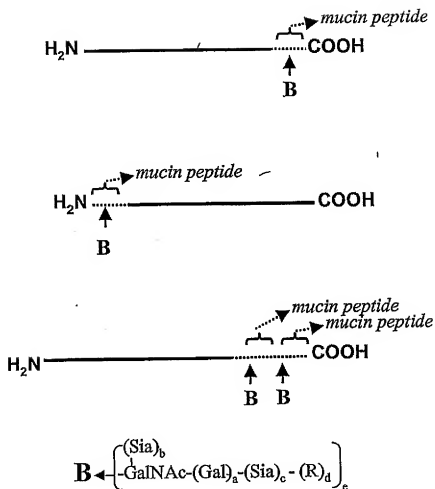


FIG. 45D

208/345



a-c, e (independently selected) = 0 or 1;
 d = 0;
 R = modifying group, mannose, oligo-
 mannose.

FIG. 45E

209/345

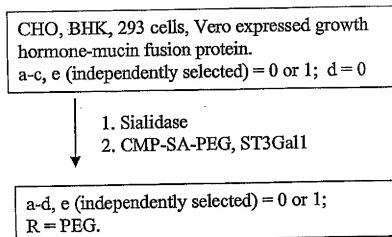


FIG. 45F

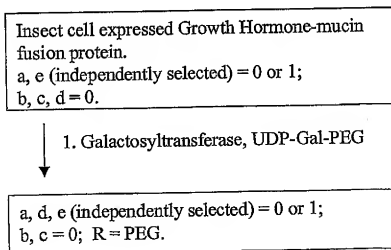


FIG. 45G

210/345

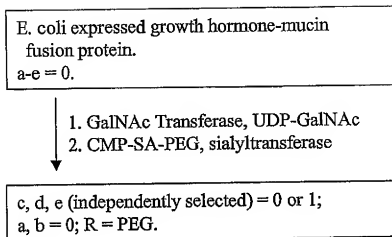


FIG. 45H

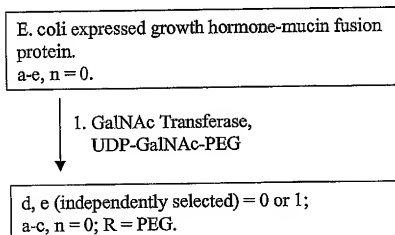


FIG. 45I

211/345

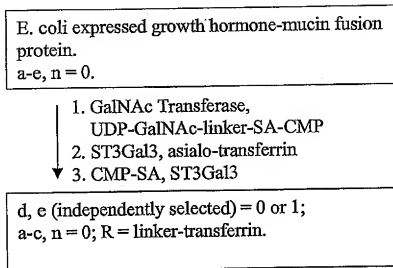


FIG. 45J

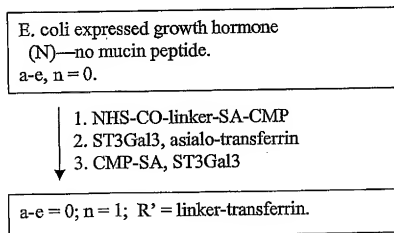
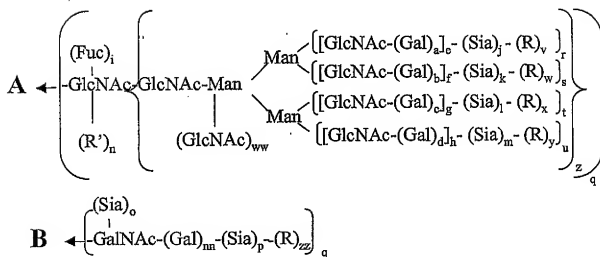
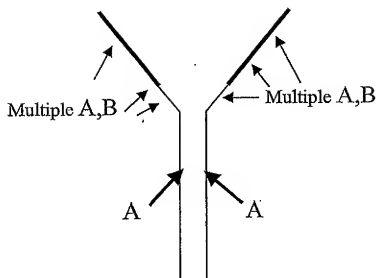


FIG. 45K

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a-d, i-m, q-u, w, z, nn, ww, zz (independently selected) = 0 or 1.

e-h (independently selected) = 0 to 4.

n, v-y = 0;

R = modifying group, mannose, oligo-mannose;

R' = H, glycosyl residue, modifying group, glycoconjugate.

FIG. 46A

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CHO, BHK, 293 cells, Vero or transgenic animals
expressed TNF Receptor IgG Fusion.
a-m, o-u, aa (independently selected) = 0 or 1;
n = 1; v-z = 0.

- ↓
1. CMP-SA, ST3Gal1
 2. galactosyltransferase, UPD-Gal
 3. CMP-SA-PEG, ST3Gal3

a-m, o-u, v-y, aa (independently selected) = 0 or 1;
n = 1; z = 0; R = PEG.

FIG. 46B

CHO, BHK, 293 cells, Vero expressed
TNF Receptor IgG Fusion.
a-m, o-u, aa (independently selected) = 0 or 1;
n = 1; v-z = 0.

- ↓
1. sialidase
 2. CMP-SA-PEG, ST3Gal1

a-i, p-u, z, aa (independently selected) = 0 or 1;
n = 1; o, j-m, v-y = 0; R = PEG.

FIG. 46C

214/345

CHO, BHK, 293 cells, Vero expressed
TNF Receptor IgG Fusion.
a-m, o-u, aa (independently selected) = 0 or 1;
n = 1; v-z = 0.



1. galactosyltransferase, UPD-Gal-PEG

a-m, o-u, v-y, aa (independently selected) = 0 or 1;
n = 1; z = 0; R = PEG.

FIG. 46D

CHO, BHK, 293 cells, Vero or transgenic animals
expressed TNF Receptor IgG Fusion.
a-m, o-u, aa (independently selected) = 0 or 1;
n = 1; v-z = 0.



1. CMP-SA, ST3Gal1

2. galactosyltransferase, UPD-Gal-PEG

a-m, o-u, v-y, aa (independently selected) = 0 or 1;
n = 1; z = 0; R = PEG.

FIG. 46E

215/345

CHO, BHK, 293 cells, Vero or transgenic animals
expressed TNF Receptor IgG Fusion.
a-m, o-u, aa (independently selected) = 0 or 1;
n = 1; v-z = 0.

- ↓
1. CMP-SA-levulinate, ST3Gal1
 2. H_4N_2 -PEG

a-m, o-u, v-y, aa (independently selected) = 0 or 1;
n = 1; z = 0; R = PEG.

FIG. 46F

CHO, BHK, 293 cells, Vero expressed
TNF Receptor IgG Fusion.
a-m, o-u, aa (independently selected) = 0 or 1;
n = 1; v-z = 0.

- ↓
1. CMP-SA-PEG, $\alpha 2,8$ -ST

a-i, o, q-u, v-z, aa (independently selected) = 0 or 1;
n = 1; j-m, p (independently selected) = 0 to 2;
v-z (independently selected) = 1,
when j-m, p (independently selected) is 2;
R = PEG.

FIG. 46G

217/345

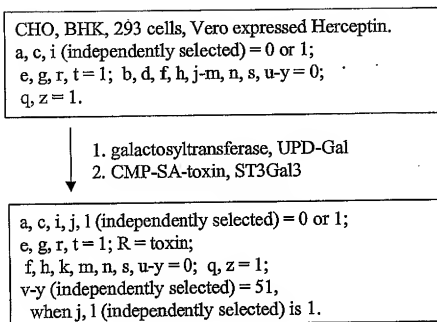


FIG. 47B

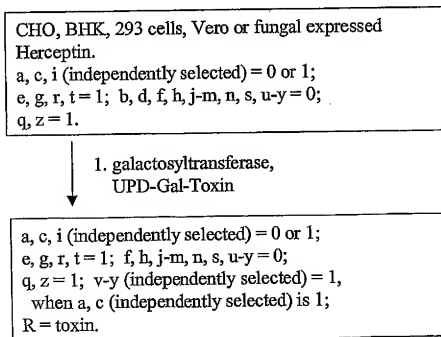


FIG. 47C

218/345

Fungi expressed Herceptin.

e, g, i, r, t (independently selected) = 0 or 1;

a-d, f, h, j-m, n, s, u-y = 0; q, z = 1.

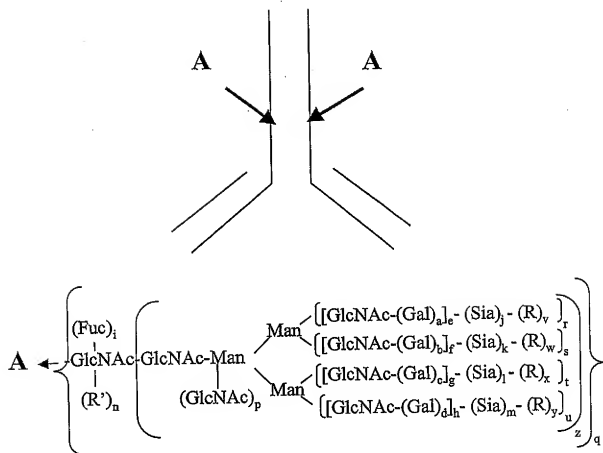
1. Endo-H
2. Galactosyltransferase, UDP-Gal
- ↓ 3.. CMP-SA-radioisotope complex, ST3Gal3

a-m, r-z = 0; q, n = 1;

R' = -Gal-Sia-radioisotope complex.

FIG. 47D

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a-d, i, p-u, (independently selected) = 0 or 1.

e-h (independently selected) = 0 to 4.

j-m (independently selected) = 0 or 1.

n, v-y = 0; z = 0 or 1;

R = polymer, toxin, radioisotope-complex, drug, mannose, oligo-mannose.

R' = H, glycosyl residue, modifying group, glycoconjugate.

FIG. 48A

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CHO, BHK, 293 cells, Vero expressed Synagis.
 a, c, i (independently selected) = 0 or 1;
 e, g, r, t = 1;
 b, d, f, h, j-m, n, s, u-y = 0; q, z = 1.

- ↓
1. galactosyltransferase, UPD-Gal
 2. CMP-SA-PEG, ST3Gal3

a, c, i, j, w, (independently selected) = 0 or 1;
 e, g, r, t = 1; f, h, k, m, n, s, u-y = 0;
 q, z = 1; v-y (independently selected) = 1,
 when j, l (independently selected) is 1;
 R = PEG.

FIG. 48B

CHO, BHK, 293 cells, Vero or fungal expressed Synagis.
 a, c, i (independently selected) = 0 or 1;
 e, g, r, t = 1; b, d, f, h, j-m, n, s, u-y = 0;
 q, z = 1.

- ↓
1. galactosyltransferase,
UPD-Gal-PEG

a, c, i, w (independently selected) = 0 or 1;
 e, g, r, t = 1; f, h, j-m, n, s, u-y = 0;
 q, z = 1; v-y (independently selected) = 1,
 when a, c (independently selected) is 1;
 R = PEG.

FIG. 48C

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Fungi expressed Synagis.

e, g, i, r, t (independently selected) = 0 or 1;

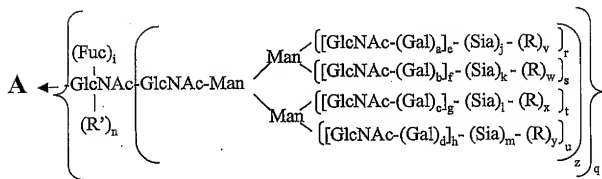
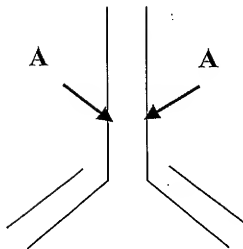
a-d, f, h, j-m, n, s, u-y = 0; q, z = 1.

- ↓ 1. Endo-H
2. Galactosyltransferase, UDP-Gal
3.. CMP-SA-PEG, ST3Gal3

a-m, r-z= 0; q, n = 1; R' = -Gal-Sia-PEG.

FIG. 48D

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a-d, i, q-u, w (independently selected) = 0 or 1.

e-h (independently selected) = 0 to 6.

j-m (independently selected) = 0 to 20.

n, v-y = 0; z = 0 or 1;

R = polymer, toxin, radioisotope-complex, drug, mannose, oligo-mannose.

R' = H, glycosyl residue, modifying group, glycoconjugate.

FIG. 49A

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CHO, BHK, 293 cells, Vero expressed Remicade.

a, c, i (independently selected) = 0 or 1;
e, g, r, t = 1; b, d, f, h, j-m, n, s, u-y = 0;
q, z = 1.

- ↓
1. galactosyltransferase, UPD-Gal
 2. CMP-SA-PEG, ST3Gal3

a, c, i, j, l (independently selected) = 0 or 1;
e, g, r, t = 1; f, h, k, m, n, s, u-y = 0;
q, z = 1; v-y (independently selected) = 1,
when j, l (independently selected) is 1;
R = PEG.

FIG. 49B

CHO, BHK, 293 cells, Vero or fungal expressed Remicade.

a, c, i (independently selected) = 0 or 1;
e, g, r, t = 1; b, d, f, h, j-m, n, s, u-y = 0;
q, z = 1.

- ↓
1. galactosyltransferase,
UPD-Gal-PEG

a, c, i (independently selected) = 0 or 1;
e, g, r, t = 1; f, h, j-m, n, s, u-y = 0;
q, z = 1; v-y (independently selected) = 1,
when a, c (independently selected) is 1;
R = PEG.

FIG. 49C

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Fungi expressed Remicade.

e, g, i, r, t (independently selected) = 0 or 1;

a-d, f, h, j-m, n, s, u-y = 0; q, z = 1.

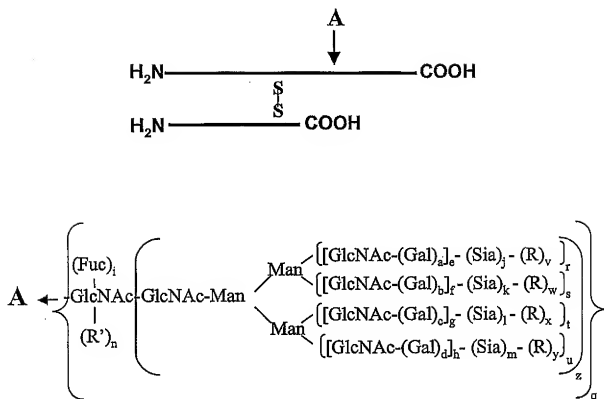
- ↓
1. Endo-H
 2. Galactosyltransferase, UDP-Gal
 - 3.. CMP-SA-radioisotope complex, ST3Gal3

a-m, r-z = 0; q, n = 1;

R' = -Gal-Sia-radioisotope complex.

FIG. 49D

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a-d, i, q-u (independently selected) = 0 or 1.

e-h (independently selected) = 0 to 4.

j-m (independently selected) = 0 or 1.

n, v-y = 0; z = 0 or 1;

R = modifying group, mannose, oligo-mannose;

R' = H, glycosyl residue, modifying group,
glycoconjugate.

FIG. 50A

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CHO, BHK, 293 cells, Vero expressed Reopro.
a-m, r-u (independently selected) = 0 or 1;
n = 0; v-y = 0; z = 1.

- ↓
1. Sialidase
 2. CMP-SA-PEG, ST3Gal3

a-m, r-u (independently selected) = 0 or 1;
v-y (independently selected) = 1,
when j-m (independently selected) is 1;
n = 0; R = PEG; z = 1.

FIG. 50B

Insect cell expressed Reopro.
a-h, j-n, s-y = 0; i, r (independently selected) = 0 or 1;
z = 1.

- ↓
1. GNT's 1&2, UDP-GlcNAc-PEG

a-d, f, h, j-n, s, u, w, y = 0;
e, g, i, r, t, v, x (independently selected) = 0 or 1;
v, x (independently selected) = 1,
when e, g (independently selected) is 1;
z = 1; R = PEG.

FIG. 50C

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Yeast expressed Reopro.

a-n = 0; r-y (independently selected) = 0 to 1;

z = 1;

R (branched or linear) = Man, oligomannose or polysaccharide.

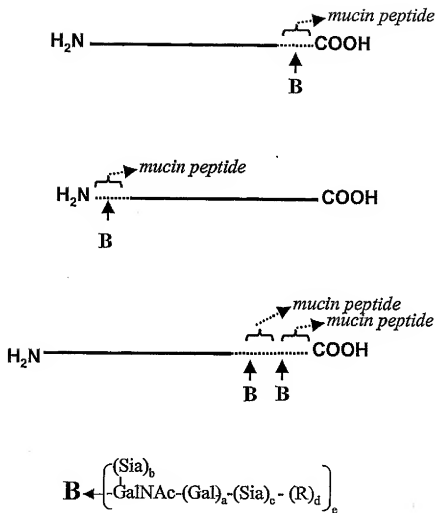
1. Endo-H

2. Galactosyltransferase, UDP-Gal-PEG

a-m, r-z = 0; n = 1; R' = -Gal-PEG.

FIG. 50D

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a-c, e (independently selected) = 0 or 1;
d = 0; R = polymer

FIG. 50E

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CHO, BHK, 293 cells, Vero expressed
Reopro-mucin fusion protein.
a-c, e (independently selected) = 0 or 1; d = 0



1. Sialidase
2. CMP-SA-PEG, ST3Gal1

a-d, e (independently selected) = 0 or 1; R = PEG.

FIG. 50F

Insect cell expressed Reopro-mucin fusion protein.
a, e (independently selected) = 0 or 1; b, c, d = 0.



1. Galactosyltransferase, UDP-Gal-PEG

a, d, e (independently selected) = 0 or 1;
b, c = 0; R = PEG.

FIG. 50G

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E. coli expressed Reopro-mucin fusion protein.
a-e = 0.

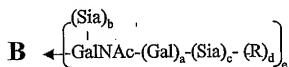
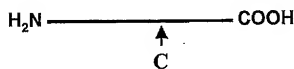
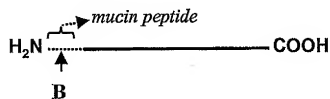
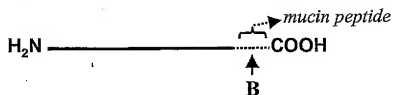


1. GalNAc Transferase, UDP-GalNAc
2. CMP-SA-PEG, sialyltransferase

c, d, e (independently selected) = 0 or 1;
a, b = 0; R = PEG.

FIG. 50H

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a-c, e (independently selected) = 0 or 1;
d = 0; R = polymer, linker.

FIG. 50I

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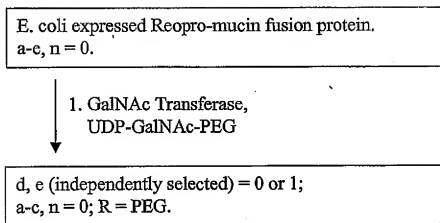


FIG. 50J

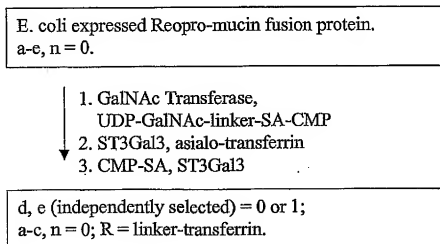


FIG. 50K

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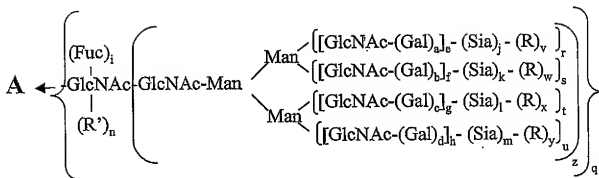
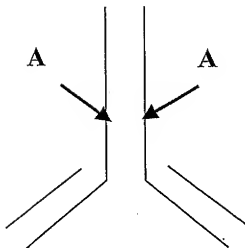
E. coli expressed Reopro(N)—no mucin peptide.
a-e, n = 0.

- ↓
1. NHS-CO-linker-SA-CMP
 2. ST3Gal3, asialo-transferrin
 3. CMP-SA, ST3Gal3

a-e = 0; n = 1; R' = linker-transferrin.

FIG. 50L

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a-d, i, q-u (independently selected) = 0 or 1.

e-h (independently selected) = 0 to 4.

j-m (independently selected) = 0 or 1.

n, v-y = 0; z = 0 or 1; R = polymer, toxin, radioisotope-complex, drug, glycoconjugate.

R' = H, sugar, glycoconjugate.

z

FIG. 51A

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CHO, BHK, 293 cells, Vero or transgenic animal
expressed Rituxan.

a, c, i (independently selected) = 0 or 1;

e, g, r, t = 1; b, d, f, h, j-m, n, s, u-y = 0; q, z = 1.



1. galactosyltransferase, UPD-Gal

2. CMP-SA-toxin, ST3Gal3

a, c, i, j, l (independently selected) = 0 or 1;

e, g, r, t = 1;

f, h, k, m, n, s, u-y = 0; q, z = 1;

v-y (independently selected) = 1,

when j, l (independently selected) is 1;

R = toxin.

FIG. 51B

CHO, BHK, 293 cells, Vero or fungal expressed
Rituxan.

a, c, e, g, i, r, t (independently selected) = 0 or 1;

b, d, f, h, j-m, n, s, u-y = 0; q, z = 1.



1. galactosyltransferase,

UPD-Gal-drug

a, c, i (independently selected) = 0 or 1;

e, g, r, t = 1; f, h, j-m, n, s, u-y = 0; q, z = 1;

v-y (independently selected) = 1,

when a, c (independently selected) is 1;

R = toxin.

FIG. 51C

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Fungi expressed Rituxan.

e, g, i, r, t (independently selected) = 0 or 1;

a-d, f, h, j-m, n, s, u-y = 0; q, z = 1.

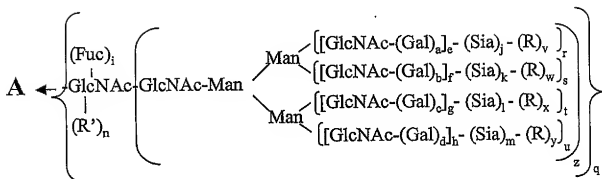
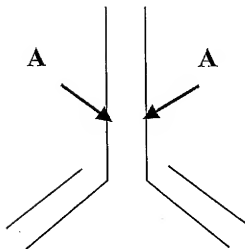
1. Endo-H
2. Galactosyltransferase, UDP-Gal
- ↓ 3. CMP-SA-radioisotope complex, ST3Gal3

a-m, r-z = 0; q, n = 1;

R' = -Gal-Sia-radioisotope complex.

FIG. 51D

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a-d, i, q-u (independently selected) = 0 or 1.

e-h (independently selected) = 0 to 4.

j-m (independently selected) = 0 or 1.

n, v-y = 0; z = 0 or 1;

R = polymer, toxin, radioisotope-complex, drug,
glycoconjugate, mannose, oligo-mannose.

R' = H, glycosyl residue, modifying group, glycoconjugate.

FIG. 51E

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CHO, BHK, 293 cells, Vero or transgenic animal
expressed Rituxan.

a, c, i (independently selected) = 0 or 1;
e, g, r, t = 1; b, d, f, h, j-m, n, s, u-y = 0;
q, z = 1.

- ↓
1. galactosyltransferase, UPD-Gal
 2. CMP-SA-PEG, ST3Gal3

a, c, i, j, l (independently selected) = 0 or 1;
e, g, r, t = 1; f, h, k, m, n, s, u-y = 0;
q, z = 1; v-y (independently selected) = 1,
when j, l (independently selected) is 1;
R = PEG.

FIG. 51F

Fungi, yeast or CHO expressed Rituxan.

e, g, i, r, t, v, x (independently selected) = 0 or 1;
a-d, f, h, j-m, n, s, u, w, y = 0; q, z = 1;
R (independently selected) = mannose, oligomannose,
polymannose.

- ↓
1. mannosidases (alpha and beta)
 2. GNT-I,II, UDP-GlcNAc
 3. Galactosyltransferase, UDP-Gal-radioisotope

a-m, r-z = 0; q, n = 1;
R' = -Gal-radioisotope complex.

FIG. 51G

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FIG. 52A

ACCCCCCTGGGCCCTGCCAGCTCCCTGCCCCAGAGCTTCCTGCTCAAT
GCTTAGAGCAAGTGAGGAAGATCCAGGGCGATGGCGCAGCGCTCCAG
GAGAAGCTGTGTGCCACCTACAAGCTGTGCCACCCGAGGAGCTGGT
GCTGCTCGGACACTCTCTGGGCATCCCCTGGGCTCCCCTGAGCAGTG
CCCCAGCCAGGCCCTGCAGCTGGCAGGCTGCTTGAGCCAACTCCATA
GCGGCCTTTTCTCTACCCAGGGGCTCCTGCAGGCCCTGGAAGGGATCT
CCCCCGAGTTGGGTCCCACCTTGGACACACTGCAGCTGGACGTCGCCG
ACTTTGCCACCACCATCTGGCAGCAGATGGAAGAACTGGGAATGGCC
CCTGCCCTGCAGCCCACCCAGGGTGCCATGCCGGCCTTCGCCTCTGCT
TTCCAGCGCCGGGCAGGAGGGGTCTGTTGCCCTCCCATCTGCAGAG
CTTCTCGGAGGTGTCGTACCGCGTTCTACGCCACCTTGCCCAGCCCTG
A

FIG. 52B

Thr Pro Leu Gly Pro Ala Ser Ser Leu Pro Gln Ser Phe Leu Leu Lys Cys Leu Glu
Gln Val Arg Lys Ile Gln Gly Asp Gly Ala Ala Leu Gln Glu Lys Leu Cys Ala Thr
Tyr Lys Leu Cys His Pro Glu Glu Leu Val Leu Leu Gly His Ser Leu Gly Ile Pro
Trp Ala Pro Leu Ser Ser Cys Pro Ser Gln Ala Leu Gln Leu Ala Gly Cys Leu Ser
Gln Leu His Ser Gly Leu Phe Leu Tyr Gln Gly Leu Leu Gln Ala Leu Glu Gly Ile
Ser Pro Glu Leu Gly Pro Thr Leu Asp Thr Leu Gln Leu Asp Val Ala Asp Phe
Ala Thr Thr Ile Trp Gln Gln Met Glu Glu Leu Gly Met Ala Pro Ala Leu Gln Pro
Thr Gln Gly Ala Met Pro Ala Phe Ala Ser Ala Phe Gln Arg Arg Ala Gly Gly Val
Leu Val Ala Ser His Leu Gln Ser Phe Leu Glu Val Ser Tyr Arg Val Leu Arg His
Leu Ala Gln Pro

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FIG. 53B

Met Ala Leu Thr Phe Ala Leu Leu Val Ala Leu Leu Val Leu Ser Cys Lys Ser
Ser Cys Ser Val Gly Cys Asp Leu Pro Gln Thr His Ser Leu Gly Ser Arg Arg Thr
Leu Met Leu Leu Ala Gln Met Arg Arg Ile Ser Leu Phe Ser Cys Leu Lys Asp
Arg His Asp Phe Gly Phe Pro Gln Glu Glu Phe Gly Asn Gln Phe Gln Lys Ala
Glu Thr Ile Pro Val Leu His Glu Met Ile Gln Gln Ile Phe Asn Leu Phe Ser Thr
Lys Asp Ser Ser Ala Ala Trp Asp Glu Thr Leu Leu Asp Lys Phe Tyr Thr Glu
Leu Tyr Gln Gln Leu Asn Asp Leu Glu Ala Cys Val Ile Gln Gly Val Gly Val
Thr Glu Thr Pro Leu Met Lys Glu Asp Ser Ile Leu Ala Val Arg Lys Tyr Phe
Gln Arg Ile Thr Leu Tyr Leu Lys Glu Lys Lys Tyr Ser Pro Cys Ala Trp Glu Val
Val Arg Ala Glu Ile Met Arg Ser Phe Ser Leu Ser Thr Asn Leu Gln Glu Ser Leu
Arg Ser Lys Glu

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FIG. 54A

ATGACCAACAAGTGTCTCCTCCAAATTGCTCTCCTGTTGTGCTTCTCC
ACTACAGCTCTTTCCATGAGCTACAACCTTGCTTGGATTCTACAAAGA
AGCAGCAATTTTCAGTGTGAGGAGCTCCTGTGGCAATTGAATGGGAG
GCTTGAATATTGCCTCAAGGACAGGATGAACTTTGACATCCCTGAGG
AGATTAAGCAGCTGCAGCAGTTCAGAAAGGAGGACGCCGATTGACC
ATCTATGAGATGCTCCAGAACATCTTTGCTATTTTCAGACAAGATTCA
TCTAGCACTGGCTGGAATGAGACTATTGTTGAGAACCTCCTGGCTAA
TGTCTATCATCAGATAAACCATCTGAAGACAGTCCTGGAAGAAAAAC
TGGAGAAAGAAGATTTTACCAGGGGAAAACTCATGAGCAGTCTGCAC
CTGAAAAGATATTATGGGAGGATTCTGCATTACCTGAAGGCCAAGGA
GTACAGTCACTGTGCCTGGACCATAGTCAGAGTGGAAATCCTAAGGA
ACTTTTACTTCATTAACAGACTTACAGGTTACCTCCGAAACTGAAGAT
CTCCTAGCCTGTCCCTCTGGGACTGGACAATTGCTTCAAGCATTCTTC
AACCAGCAGATGCTGTTTAAAGTGACTGATGGCTAATGTACTGCAAAT
GAAAGGACACTAGAAGATTTTGAAATTTTATTAAATTATGAGTTATT
TTTATTTAT TTAAATTTTATTTTGAAAATAAATTATTTTGGTG

FIG. 54B

Met Thr Asn Lys Cys Leu Leu Gln Ile Ala Leu Leu Leu Cys Phe Ser Thr Thr Ala
Leu Ser Met Ser Tyr Asn Leu Leu Gly Phe Leu Gln Arg Ser Ser Asn Phe Gln
Cys Gln Lys Leu Leu Trp Gln Leu Asn Gly ArgLeu Glu Tyr Cys Leu Lys Asp
Arg Met Asn Phe Asp Ile Pro Glu Glu Ile Lys Gln Leu Gln Gln Phe Gln Lys Glu
Asp Ala Ala Leu Thr Ile Tyr Glu Met Leu Gln Asn Ile Phe Ala Ile Phe Arg Gln
Asp Ser Ser Ser Thr Gly Trp Asn Glu Thr Ile Val Glu Asn Leu Leu Ala Asn Val
Tyr His Gln Ile Asn His Leu Lys Thr Val Leu Glu Glu Lys Leu Glu Lys Glu Asp
Phe Thr Arg Gly Lys Leu Met Ser Ser Leu His Leu Lys Arg Tyr Tyr Gly Arg Ile
Leu His Tyr Leu Lys Ala Lys Glu Tyr Ser His Cys Ala Trp Thr Ile Val Arg Val
Glu Ile Leu Arg Asn Phe Tyr Phe Ile Asn Arg Leu Thr Gly Tyr Leu Arg Asn

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FIG. 55A

ATGGTCTCCCCAGGCCCTCAGGCTCCTCTGCCTTCTGCTTGGGCTTCAG
GGCTGCCTGGCTGCAGTCTTCGTAACCCAGGAGGAAGCCACGGCGT
CCTGCACCGGCGCCGGCGCGCAACCGCTTCTGGAGGAGCTGCGGC
CGGGCTCCCTGGAGAGGGAGTGCAAGGAGGAGCAGTGCTCCTTCGA
GGAGGCCCCGGGAGATCTTCAAGGACGCGGAGAGGACGAAGCTGTTC
TGGATTTCTTACAGTGATGGGGACCAGTGTGCCTCAAGTCCATGCCA
GAATGGGGGCTCCTGCAAGGACCAGCTCCAGTCCTATATCTGCTTCT
GCCTCCCTGCCCTTCGAGGGCCGGAACCTGTGAGACGCACAAGGATGAC
CAGCTGATCTGTGTGAACGAGAACGGCGGCTGTGAGCAGTACTGCAG
TGACCACACGGGCACCAAGCGCTCCTGTCCGTGCCACGAGGGGTACT
CTCTGCTGGCAGACGGGGTGTCTTGACACCCACAGTTGAATATCCA
TGTGGA AAAAATACCTATTCTAGAAAAAAGAAATGCCAGCAAAACCCCA
AGGCCGAATTGTGGGGGGCAAGGTGTGCCCCAAAGGGGAGTGTCCA
TGGCAGGTCCTGTTGTTGGTGAATGGAGCTCAGTTGTGTGGGGGGAC
CCTGATCAACACCATCTGGGTGGTCTCCGCGGCCCACTGTTTCGACAA
AATCAAGAACTGGAGGAACCTGATCGCGGTGCTGGGCGAGCACGAC
CTCAGCGAGCACGACGGGGATGAGCAGAGCCGGCGGGTGGCGCAGG
TCATCATCCCCAGCACGTACGTCCCGGGCACCAACCAACGACATC
GCGCTGCTCCGCTGCACCAAGCCCGTGGTCCTCACTGACCATGTGGTG
CCCCCTGCGCTGCCCCGAACGGACGTTCTCTGAGAGGACGCTGGCCTTC
GTGCGCTTCTCATTGGTACGCGGCTGGGGCCAGCTGCTGGACCGTGG
CGCCACGGCCCTGGAGCTCATGGTGCTCAACGTGCCCCGGCTGATGA
CCCAGGACTGCCTGCAGCAGTCACGGAAGGTGGGAGACTCCCCAAAT
ATCACGGAGTACATGTTCTGTGCCGGCTACTCGGATGGCAGCAAGGA
CTCCTGCAAGGGGGACAGTGGAGGCCCACATGCCACCCACTACCGGG
GCACGTGGTACCTGACGGGCATCGTCAGCTGGGGCCAGGGCTGCGCA
ACCGTGGGCCACTTTGGGGGTGTACACCAGGGTCTCCAGTACATCGA
GTGGCTGCAAAAGCTCATGCGCTCAGAGCCACGCCCAGGAGTCCTCC
TGCGAGCCCCATTCCC

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FIG. 55B

Met Val Ser Gln Ala Leu Arg Leu Leu Cys Leu Leu Leu Gly Leu Gln Gly Cys
Leu Ala Ala Val Phe Val Thr Gln Glu Ala His Gly Val Leu His Arg Arg Arg
Arg Ala Asn Ala Phe Leu Glu Glu Leu Arg Pro Gly Ser Leu Glu Arg Glu Cys
Lys Glu Glu Gln Cys Ser Phe Glu Glu Ala Arg Glu Ile Phe Lys Asp Ala Glu Arg
Thr Lys Leu Phe Trp Ile Ser Tyr Ser Asp Gly Asp Gln Cys Ala Ser Ser Pro Cys
Gln Asn Gly Gly Ser Cys Lys Asp Gln Leu Gln Ser Tyr Ile Cys Phe Cys Leu Pro
Ala Phe Glu Gly Arg Asn Cys Glu Thr His Lys Asp Asp Gln Leu Ile Cys Val
Asn Glu Asn Gly Gly Cys Glu Gln Tyr Cys Ser Asp His Thr Gly Thr Lys Arg
Ser Cys Arg Cys His Glu Gly Tyr Ser Leu Leu Ala Asp Gly Val Ser Cys Thr Pro
Thr Val Glu Tyr Pro Cys Gly Lys Ile Pro Ile Leu Glu Lys Arg Asn Ala Ser Lys
Pro Gln Gly Arg Ile Val Gly Gly Lys Val Cys Pro Lys Gly Glu Cys Pro Trp Gln
Val Leu Leu Leu Val Asn Gly Ala Gln Leu Cys Gly Gly Thr Leu Ile Asn Thr Ile
Trp Val Val Ser Ala Ala His Cys Phe Asp Lys Ile Lys Asn Trp Arg Asn Leu Ile
Ala Val Leu Gly Glu His Asp Leu Ser Glu His Asp Gly Asp Glu Gln Ser Arg
Arg Val Ala Gln Val Ile Ile Pro Ser Thr Tyr Val Pro Gly Thr Thr Asn His Asp
Ile Ala Leu Leu Arg Leu His Gln Pro Val Val Leu Thr Asp His Val Val Pro Leu
Cys Leu Pro Glu Arg Thr Phe Ser Glu Arg Thr Leu Ala Phe Val Arg Phe Ser
Leu Val Ser Gly Trp Gly Gln Leu Leu Asp Arg Gly Ala Thr Ala Leu Glu Leu
Met Val Leu Asn Val Pro Arg Leu Met Thr Gln Asp Cys Leu Gln Gln Ser Arg
Lys Val Gly Asp Ser Pro Asn Ile Thr Glu Tyr Met Phe Cys Ala Gly Tyr Ser Asp
Gly Ser Lys Asp Ser Cys Lys Gly Asp Ser Gly Gly Pro His Ala Thr His Tyr Arg
Gly Thr Trp Tyr Leu Thr Gly Ile Val Ser Trp Gly Gln Gly Cys Ala Thr Val Gly
His Phe Gly Val Tyr Thr Arg Val Ser Gln Tyr Ile Glu Trp Leu Gln Lys Leu Met
Arg Ser Glu Pro Arg Pro Gly Val Leu Leu Arg Ala Pro Phe Pro

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FIG. 56A

ATGCAGCGCGTGAACATGATCATGGCAGAATCACCAAGCCTCATCAC
CATCTGCCCTTTAGGATATCTACTCAGTGCTGAATGTACAGTTTCTT
GATCATGAAAACGCCAACAAAATTCTGAATCGGCCAAAGAGGTATAA
TTCAGGTAAATTGGAAGAGTTTGTTC AAGGGAACCTTGAGAGAGAAT
GTATGGAAGAAAAGTGTAGTTTGAAGAACCACGAGAAGTTTTTGAA
AACACTGAAAAGACAACCTGAATTTGGAAGCAGTATGTTGATGGAGA
TCAGTGTGAGTCCAATCCATGTTTAAATGGCGGCAGTTGCAAGGATG
ACATTAATTCCTATGAATGTTGGTGTCCCTTTGGATTTGAAGGAAAGA
ACTGTGAATTAGATGTAACATGTAACATTAAGAATGGCAGATGCGAG
CAGTTTTGTAAAAATAGTGCTGATAACAAGGTGGTTTGCTCCTGTACT
GAGGGATATCGACTTGCAGAAAACCAGAAGTCCTGTGAACCAGCAGT
GCCATTTCCATGTGGAAGAGTTTCTGTTTCACAAACTTCTAAGCTCAC
CCGTGCTGAGGCTGTTTTTCTGTATGTGGACTATGTAAATCCTACTGA
AGCTGAAACCATTTTGGATAACATCACTCAAGGCACCCAATCATTTA
ATGACTTCACCTCGGGTTGTTGGTGGAGAAGATGCCAAACCAGGTCAA
TTCCCTTGGCAGGTTGTTTTGAATGGTAAAGTTGATGCATTCTGTGGA
GGCTCTATCGTTAATGAAAAATGGATTGTAAGTGTGCTGCCACTGTGTT
GAAACTGGTGTAAAAATTACAGTTGTGCGCAGGTGAACATAATATTGA
GGAGACAGAACATACAGAGCAAAAAGCGAAATGTGATTTCGAGCAATT
ATTCCTCACCACAACATACAATGCAGCTATTAATAAGTACAACCATGA
CATTGCCCTTCTGGAAGCTGGACGAACCCCTIAGTGCTAAACAGCTACG
TTACACCTATTTCGATTGCTGACAAGGAATACACGAACATCTTCTCTCA
AATTTGGATCTGGCTATGTAAGTGGCTGGGCAAGAGTCTTCCACAAA
GGGAGATCAGCTTTAGTTCCTCAGTACCTTAGAGTTCCACTTGTTGAC
CGAGCCACATGTCTTCGATCTACAAAGTTCACCATCTATAACAACAT
GTTCTGTGCTGGCTTCCATGAAGGAGGTAGAGATTTCATGTCAAGGAG
ATAGTGGGGGACCCCATGTTACTGAAGTGGGAAGGACCAGTTTCTTA
ACTGGAATTATTAGCTGGGGTGAAGAGTGTGCAATGAAAGGCAAATA
TGGAATATATACCAAGGTATCCCGGTATGTCAACTGGATTAAAGGAAA
AAACAAAGCTCACTTAATGAAAGATGGATTTC AAGGTTAATTCATT
GGAATTGAAAATTAACAG

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FIG. 56B

Met Gln Arg Val Asn Met Ile Met Ala Glu Ser Pro Ser Leu Ile Thr Ile Cys Leu
Leu Gly Tyr Leu Leu Ser Ala Glu Cys Thr Val Phe Leu Asp His Glu Asn Ala
Asn Lys Ile Leu Asn Arg Pro Lys Arg Tyr Asn Ser Gly Lys Leu Glu Glu Phe
Val Gln Gly Asn Leu Glu Arg Glu Cys Met Glu Glu Lys Cys Ser Phe Glu Glu
Pro Arg Glu Val Phe Glu Asn Thr Glu Lys Thr Thr Glu Phe Trp Lys Gln Tyr
Val Asp Gly Asp Gln Cys Glu Ser Asn Pro Cys Leu Asn Gly Gly Ser Cys Lys
Asp Asp Ile Asn Ser Tyr Glu Cys Trp Cys Pro Phe Gly Phe Glu Gly Lys Asn
Cys Glu Leu Asp Val Thr Cys Asn Ile Lys Asn Gly Arg Cys Glu Gln Phe Cys
Lys Asn Ser Ala Asp Asn Lys Val Val Cys Ser Cys Thr Glu Gly Tyr Arg Leu
Ala Glu Asn Gln Lys Ser Cys Glu Pro Ala Val Pro Phe Pro Cys Gly Arg Val Ser
Val Ser Gln Thr Ser Lys Leu Thr Arg Ala Glu Ala Val Phe Pro Asp Val Asp Tyr
Val Asn Pro Thr Glu Ala Glu Thr Ile Leu Asp Asn Ile Thr Gln Gly Thr Gln Ser
Phe Asn Asp Phe Thr Arg Val Val Gly Gly Glu Asp Ala Lys Pro Gly Gln Phe
Pro Trp Gln Val Val Leu Asn Gly Lys Val Asp Ala Phe Cys Gly Gly Ser Ile Val
Asn Glu Lys Trp Ile Val Thr Ala Ala His Cys Val Glu Thr Gly Val Lys Ile Thr
Val Val Ala Gly Glu His Asn Ile Glu Glu Thr Glu His Thr Glu Gln Lys Arg Asn
Val Ile Arg Ala Ile Ile Pro His His Asn Tyr Asn Ala Ala Ile Asn Lys Tyr Asn
His Asp Ile Ala Leu Leu Glu Leu Asp Glu Pro Leu Val Leu Asn Ser Tyr Val Thr
Pro Ile Cys Ile Ala Asp Lys Glu Tyr Thr Asn Ile Phe Leu Lys Phe Gly Ser Gly
Tyr Val Ser Gly Trp Ala Arg Val Phe His Lys Gly Arg Ser Ala Leu Val Leu Gln
Tyr Leu Arg Val Pro Leu Val Asp Arg Ala Thr Cys Leu Arg Ser Thr Lys Phe
Thr Ile Tyr Asn Asn Met Phe Cys Ala Gly Phe His Glu Gly Gly Arg Asp Ser
Cys Gln Gly Asp Ser Gly Gly Pro His Val Thr Glu Val Glu Gly Thr Ser Phe Leu
Thr Gly Ile Ile Ser Trp Gly Glu Glu Cys Ala Met Lys Gly Lys Tyr Gly Ile Tyr
Thr Lys Val Ser Arg Tyr Val Asn Trp Ile Lys Glu Lys Thr Lys Leu Thr

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FIG. 57A

ATGGATTACTACAGAAAATATGCAGCTATCTTTCTGGTCACATTGTCTG
 GTGTTTCTGCATGTTCTCCATTCGGCTCCTGATGTGCAGGATTGCCCCA
 GAATGCACGCTACAGGAAAACCCATTCTTCTCCCAGCCGGGTGCCCC
 AATACTTCAGTGCATGGGCTGCTGCTTCTCTAGAGCATATCCCCTCC
 ACTAAGGTCCAAGAAGACGATGTTGGTCCAAAAGAACGTACCTCAG
 AGTCCACTTGCTGTGTAGCTAAATCATATAACAGGGTCACAGTAATG
 GGGGGTTTCAAAGTGGAGAACCACACGGCGTGCCACTGCAGTACTTG
 TTATTATCACAAATCTTAAATGTTTTACCAAGTGCTGTCTTGATGACT
 GCTGATTTTCTGGAATGGAAAATTAAGTTGTTTAGTGTTTATGGCTTT
 GTGAGATAAAACTCTCCTTTTCCTTACCATACCCTTTGACACGCTTC
 AAGGATATACTGCAGCTTTACTGCCTTCCTCCTTATCCTACAGTACAA
 TCAGCAGTCTAGTTCTTTTCATTGGAATGAATACAGCATTAAAGCTTG
 TTCCACTGCAAATAAAGCCTTTTAAATCATC

FIG. 57B

Met Asp Tyr Tyr Arg Lys Tyr Ala Ala Ile Phe Leu Val Thr Leu Ser Val Phe Leu
 His Val Leu His Ser Ala Pro Asp Val Gln Asp Cys Pro Glu Cys Thr Leu Gln Glu
 Asn Pro Phe Phe Ser Gln Pro Gly Ala Pro Ile Leu Gln Cys Met Gly Cys Cys Phe
 Ser Arg Ala Tyr Pro Thr Pro Leu Arg Ser Lys Lys Thr Met Leu Val Gln Lys Asn
 Val Thr Ser Glu Ser Thr Cys Cys Val Ala Lys Ser Tyr Asn Arg Val Thr Val Met
 Gly Gly Phe Lys Val Glu Asn His Thr Ala Cys His Cys Ser Thr Cys Tyr Tyr His
 Lys Ser

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FIG. 57C

ATGAAGACACTCCAGTTTTTCTTCCTTTTCTGTTGCTGGAAAGCAATC
TGCTGCAATAGCTGTGAGCTGACCAACATCACCATTGCAATAGAGAA
AGAAGAATGTCGTTTCTGCATAAGCATCAACACCACTGGTGTGCTG
GCTACTGCTACACCAGGGATCTGGTGTATAAAGGACCCAGCCAGGCCC
AAAATCCAGAAAACATGTACCTTCAAGGAACTGGTATATGAAACAGT
GAGAGTGCCCGGCTGTGCTCACCATGCAGATTCCTTGTATACATACCC
AGTGGCCACCCAGTGTCACTGTGGCAAGTGTGACAGCGACAGCACTG
ATTGTACTGTGCGAGGCCTGGGGCCAGCTACTGCTCCTTTGGTGAAA
TGAAAGAATAA

FIG. 57D

Met Lys Thr Leu Gln Phe Phe Phe Leu Phe Cys Cys Trp Lys Ala Ile Cys Cys
Asn Ser Cys Glu Leu Thr Asn Ile Thr Ile Ala Ile Glu Lys Glu Glu Cys Arg Phe
Cys Ile Ser Ile Asn Thr Thr Trp Cys Ala Gly Tyr Cys Tyr Thr Arg Asp Leu Val
Tyr Lys Asp Pro Ala Arg Pro Lys Ile Gln Lys Thr Cys Thr Phe Lys Glu Leu Val
Tyr Glu Thr Val Arg Val Pro Gly Cys Ala His His Ala Asp Ser Leu Tyr Thr Tyr
Pro Val Ala Thr Gln Cys His Cys Gly Lys Cys Asp Ser Asp Ser Thr Asp Cys
Thr Val Arg Gly Leu Gly Pro Ser Tyr Cys Ser Phe Gly Glu Met Lys Glu

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FIG. 58A

CCCGGAGCCGGACCGGGGCCACCGCGCCCGCTCTGCTCCGACACCGC
GCCCCCTGGACAGCCGCCCTCTCCTCCAGGCCCGTGGGGCTGGCCCT
GCACCGCCGAGCTTCCCGGATGAGGGCCCCCGGTGTGGTCAACCGG
CGCGCCCCAGGTTCGTGAGGGACCCCGCCAGGCGCGGAGATGGGG
GTGCACGAATGTCCTGCCTGGCTGTGGCTTCTCCTGTCCCTGCTGTG
CTCCCTCTGGGCCTCCCAGTCTTGGGCGCCCCACCACGCCTCATCTGT
GACAGCCGAGTCTTGGAGAGGTACCTCTTGGAGGCCAAGGAGGCCG
AGAATATCACGACGGGCTGTGCTGAACACTGCAGCTTGAATGAGAAT
ATCACTGTCCAGACACCAAAGTTAATTTCTATGCCTGGAAGAGGAT
GGAGGTCGGGCAGCAGGCCGTAGAAGTCTGGCAGGGCCTGGCCCTG
CTGTCGGAAGCTGTCTTGCAGGGGCCAGGCCCTGTTGGTCAACTCTTC
CAGCCGTGGGAGCCCCCTGCAGCTGCATGTGGATAAAGCCGTCAGTG
CCTTCGCAGCCTCACCACTCTGCTTCGGGCTCTGCGAGCCCAGAAGG
AAGCCATCTCCCCCTCCAGATGCGGCCTCAGCTGCTCCACTCCGAACA
ATCACTGCTGACACTTTCGCAAACCTCTCCGAGTCTACTCCAATTC
CTCCGGGGAAGGCTGAAGCTGTACACAGGGGAGGCCTGCAGGACAG
GGGACAGATGACCAGGTGTGTCCACCTGGGCATATCCACCACCTCCC
TCACCAACATTGCTTGTGCCACACCCTCCCCCGCCACTCCTGAACCCC
GTGAGGGGGCTCTCAGCTCAGCGCCAGCCTGTCCCATGGACACTCCA
GTGCCAGCAATGACATCTCAGGGGCCAGAGGAACTGTCCAGAGAGC
AACTCTGAGATCTAAGGATGTACAGGGCCAACTTGAGGGCCCAGAG
CAGGAAGCATTCAGAGAGCAGCTTTAAACTCAGGGACAGAGCCATG
CTGGGAAGACGCCTGAGCTCACTCGGCACCCTGCAAAATTTGATGCC
AGGACACGCTTTGGAGGCGATTACCTGTTTTGCACCTACCATCAGG
GACAGGATGACCTGGAGAACTTAGGTGGCAAGCTGTGACTTCTCCAG
GTCTCACGGGCATGGGCACTCCCTTGGTGGCAAGAGCCCCCTTGACA
CCGGGGTGGTGGGAACCATGAAGACAGGATGGGGGCTGGCCCTCTGG
CTCTCATGGGGTCCAAAGTTTGTGTATTCTTCAACCTCATTGACAAGA
ACTGAAACCACCAAAAAAAAAAAAAA

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FIG. 58B

Met Gly Val His Glu Cys Pro Ala Trp Leu Trp Leu Leu Leu Ser Leu Leu Ser
Leu Pro Leu Gly Leu Pro Val Leu Gly Ala Pro Pro Arg Leu Ile Cys Asp Ser
Arg Val Leu Glu Arg Tyr Leu Leu Glu Ala Lys Glu Ala Glu Asn Ile Thr Thr
Gly Cys Ala Glu His Cys Ser Leu Asn Glu Asn Ile Thr Val Pro Asp Thr Lys
Val Asn Phe Tyr Ala Trp Lys Arg Met Glu Val Gly Gln Gln Ala Val Glu Val
Trp Gln Gly Leu Ala Leu Leu Ser Glu Ala Val Leu Arg Gly Gln Ala Leu Leu
Val Asn Ser Ser Gln Pro Trp Glu Pro Leu Gln Leu His Val Asp Lys Ala Val Ser
Gly Leu Arg Ser Leu Thr Thr Leu Leu Arg Ala Leu Arg Ala Gln Lys Glu Ala Ile
Ser Pro Pro Asp Ala Ala Ser Ala Ala Pro Leu Arg Thr Ile Thr Ala Asp Thr Phe
Arg Lys Leu Phe Arg Val Tyr Ser Asn Phe Leu Arg Gly Lys Leu Lys Leu Tyr
Thr Gly Glu Ala Cys Arg Thr Gly Asp Arg

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FIG. 59A

ATGTGGCTGCAGAGCCTGCTGCTCTTGGGCACTGTGGCCTGCAGCAT
CTCTGCACCCGCCGCTCGCCCAGCCCCAGCACGCAGCCCTGGGAGC
ATGTGAATGCCATCCAGGAGGCCCGGCGTCTCCTGAACCTGAGTAGA
GACACTGCTGCTGAGATGAATGAAACAGTAGAAGTCATCTCAGAAAT
GTTTGACCTCCAGGAGCCGACCTGCCTACAGACCCGCGCTGGAGCTGT
ACAAGCAGGGCCTGCGGGGCAGCCTCACCAAGCTCAAGGGCCCCTTG
ACCATGATGGCCAGCCACTACAAGCAGCACTGCCCTCCAACCCCGGA
AACTTCCTGTGCAACCCAGATTATCACCTTTGAAAGTTTCAAAGAGA
ACCTGAAGGACTTTCTGCTTGTCATCCCTTTGACTGCTGGGAGCCAG
TCCAGGAGTGA

FIG. 59B

Met Trp Leu Gln Ser Leu Leu Leu Gly Thr Val Ala Cys Ser Ile Ser Ala Pro
Ala Arg Ser Pro Ser Pro Ser Thr Gln Pro Trp Glu His Val Asn Ala Ile Gln Glu
Ala Arg Arg Leu Leu Asn Leu Ser Arg Asp Thr Ala Ala Glu Met Asn Glu Thr
Val Glu Val Ile Ser Glu Met Phe Asp Leu Gln Glu Pro Thr Cys Leu Gln Thr Arg
Leu Glu Leu Tyr Lys Gln Gly Leu Arg Gly Ser Leu Thr Lys Leu Lys Gly Pro
Leu Thr Met Met Ala Ser His Tyr Lys Gln His Cys Pro Pro Thr Pro Glu Thr Ser
Cys Ala Thr Gln Ile Ile Thr Phe Glu Ser Phe Lys Glu Asn Leu Lys Asp Phe Leu
Leu Val Ile Pro Phe Asp Cys Trp Glu Pro Val Gln Glu

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FIG. 60A

ATGAAATATACAAGTTATATCTTGGCTTTTCAGCTCTGCATCGTTTTG
GGTTCCTCTGGCTGTTACTGCCAGGACCCATATGTAAAAGAAGCAGA
AAACCTTAAGAAAATATTTAATGCAGGTCATTTCAGATGTAGCGGATA
ATGGAACCTCTTTTCTTAGGCATTTTGAAGAATTGGAAAGAGGAGAGT
GACAGAAAAATAATGCAGAGCCAAATTGTCTCCTTTTACTTCAAACCT
TTTTAAAACTTTAAAGATGACCAGAGCATCCAAAAGAGTGTGGAGA
CCATCAAGGAAGACATGAATGTCAAGTTTTTCAATAGCAACAAAAAG
AAACGAGATGACTTCGAAAAGCTGACTAATTATTCGGTAACTGACTT
GAATGTCCAACGCAAAGCAATACATGAACATCCAAAGTGATGGCTG
AACTGTCGCCAGCAGCTAAAAACAGGGAAGCGAAAAAGGAGTCAGAT
GCTGTTTCGAGGTCGAAGAGCATCCAGTAA

FIG. 60B

Met Lys Tyr Thr Ser Tyr Ile Leu Ala Phe Gln Leu Cys Ile Val Leu Gly Ser Leu
Gly Cys Tyr Cys Gln Asp Pro Tyr Val Lys Glu Ala Glu Asn Leu Lys Lys Tyr
Phe Asn Ala Gly His Ser Asp Val Ala Asp Asn Gly Thr Leu Phe Leu Gly Ile
Leu Lys Asn Trp Lys Glu Glu Ser Asp Arg Lys Ile Met Gln Ser Gln Ile Val Ser
Phe Tyr Phe Lys Leu Phe Lys Asn Phe Lys Asp Asp Gln Ser Ile Gln Lys Ser Val
Glu Thr Ile Lys Glu Asp Met Asn Val Lys Phe Phe Asn Ser Asn Lys Lys Lys
Arg Asp Asp Phe Glu Lys Leu Thr Asn Tyr Ser Val Thr Asp Leu Asn Val Gln
Arg Lys Ala Ile His Glu Leu Ile Gln Val Met Ala Glu Leu Ser Pro Ala Ala Lys
Thr Gly Lys Arg Lys Arg Ser Gln Met Leu Phe Arg Gly Arg Arg Ala Ser Gln

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FIG. 61A

CTGGGACAGTGAATCGACAATGCCGTCTTCTGTCTCGTGGGGCATCCT
CCTGCTGGCAGGCCTGTGCTGCCTGGTCCCTGTCTCCCTGGCTGAGGA
TCCCCAGGGAGATGCTGCCCAGAAGACAGATACATCCCACCATGATC
AGGATCACCCAACCTTCAACAAGATCACCCCCAACCTGGCTGAGTTC
GCCTTCAGCCTATACCGCCAGCTGGCACACCAGTCCAACAGCACCAA
TATCTTCTTCTCCCCAGTGAGCATCGCTACAGCCTTTGCAATGCTCTC
CCTGGGGACCAAGGCTGACACTACGATGAAATCCTGGAGGGCCTGA
ATTTCAACCTCACGGAGATTCCGGAGGCTCAGATCCATGAAGGCTTC
CAGGAACCTCCTCCGTACCCTCAACCAGCCAGACAGCCAGCTCCAGCT
GACCACCGGCAATGGCCTGTTCCTCAGCGAGGGCCTGAAGCTAGTGG
ATAAGTTTTTTGGAGGATGTTAAAAAGTTGTACCACTCAGAAGCCTTC
ACTGTCAACTTCGGGGACACCGAAGAGGCCAAGAAACAGATCAACG
ATTACGTGGAGAAGGGTACTCAAGGGAAAATTGTGGATTTGGTCAAG
GAGCTTGACAGAGACACAGTTTTTGCTCTGGTGAATTACATCTTCTTT
AAAGGCAAATGGGAGAGACCCTTTGAAGTCAAGGACACCGAGGAAG
AGGACTTCCACGTGGACCAAGGTGACCACCGTGAAGGTGCCTATGATG
AAGCGTTTAGGCATGTTAACATCCAGCACTGTAAGAAAGCTGTCCAG
CTGGGTGCTGCTGATGAAATACCTGGGCAATGCCACCGCCATCTTCT
TCCTGCCTGATGAGGGGAAACTACAGCACCTGGAAAATGAACTCACC
CAGGATATCATCACCAGTTCTCTGGAAAATGAAGACAGAAGGTCTGC
CAGCTTACATTTACCCAAACTGTCCATTACTGGAACCTATGATCTGAA
GAGCGTCTGGGTCAACTGGGCATCACTAAGGTCTTCAGCAATGGGG
CTGACCTCTCCGGGGTCA CAGAGGAGGCACCCCTGAAGCTCTCCAAG
GCCGTGCATAAGGCTGTGCTGACCATCGACGAGAAAGGGACTGAAGC
TGCTGGGGCCATGTTTTTAGAGGCCATACCCATGTCTATCCCCCCCCGA
GGTCAAGTTCACCAAACCTTTGTCTTCTTAATGATTGAACAAAATAC
CAAGTCTCCCCCTCTTCATGGGAAAAGTGGTGAATCCCACCCAAAAAT
AACTGCCTCTCGCTCCTCAACCCCTCCCTCCATCCCTGGCCCCCTCC
CTGGATGACATTAAAGAAGGGTTGAGCTGG

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FIG. 61B

Met Pro Ser Ser Val Ser Trp Gly Ile Leu Leu Leu Ala Gly Leu Cys Cys Leu Val
Pro Val Ser Leu Ala Glu Asp Pro Gln Gly Asp Ala Ala Gln Lys Thr Asp Thr Ser
His His Asp Gln Asp His Pro Thr Phe Asn Lys Ile Thr Pro Asn Leu Ala Glu Phe
Ala Phe Ser Leu Tyr Arg Gln Leu Ala His Gln Ser Asn Ser Thr Asn Ile Phe Phe
Ser Pro Val Ser Ile Ala Thr Ala Phe Ala Met Leu Ser Leu Gly Thr Lys Ala Asp
Thr His Asp Glu Ile Leu Glu Gly Leu Asn Phe Asn Leu Thr Glu Ile Pro Glu Ala
Gln Ile His Glu Gly Phe Gln Glu Leu Leu Arg Thr Leu Asn Gln Pro Asp Ser Gln
Leu Gln Leu Thr Thr Gly Asn Gly Leu Phe Leu Ser Glu Gly Leu Lys Leu Val
Asp Lys Phe Leu Glu Asp Val Lys Lys Leu Tyr His Ser Glu Ala Phe Thr Val
Asn Phe Gly Asp Thr Glu Glu Ala Lys Lys Gln Ile Asn Asp Tyr Val Glu Lys
Gly Thr Gln Gly Lys Ile Val Asp Leu Val Lys Glu Leu Asp Arg Asp Thr Val
Phe Ala Leu Val Asn Tyr Ile Phe Phe Lys Gly Lys Trp Glu Arg Pro Phe Glu Val
Lys Asp Thr Glu Glu Glu Asp Phe His Val Asp Gln Val Thr Thr Val Lys Val
Pro Met Met Lys Arg Leu Gly Met Phe Asn Ile Gln His Cys Lys Lys Leu Ser
Ser Trp Val Leu Leu Met Lys Tyr Leu Gly Asn Ala Thr Ala Ile Phe Phe Leu Pro
Asp Glu Gly Lys Leu Gln His Leu Glu Asn Glu Leu Thr His Asp Ile Ile Thr Lys
Phe Leu Glu Asn Glu Asp Arg Arg Ser Ala Ser Leu His Leu Pro Lys Leu Ser Ile
Thr Gly Thr Tyr Asp Leu Lys Ser Val Leu Gly Gln Leu Gly Ile Thr Lys Val Phe
Ser Asn Gly Ala Asp Leu Ser Gly Val Thr Glu Glu Ala Pro Leu Lys Leu Ser Lys
Ala Val His Lys Ala Val Leu Thr Ile Asp Glu Lys Gly Thr Glu Ala Ala Gly Ala
Met Phe Leu Glu Ala Ile Pro Met Ser Ile Pro Pro Glu Val Lys Phe Asn Lys Pro
Phe Val Phe Leu Met Ile Glu Gln Asn Thr Lys Ser Pro Leu Phe Met Gly Lys Val
Val Asn Pro Thr Gln Lys

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FIG. 62A-1

GCTAACCTAGTGCCTATAGCTAAGGCAGGTACCTGCATCCTTGTTTT
GTTTAGTGGATCCTCTATCCTTCAGAGACTCTGGAACCCCTGTGGTCT
TCTCTTCATCTAATGACCCTGAGGGGATGGAGTTTTCAAGTCCTTCCA
GAGAGGAATGTCCCAAGCCTTTGAGTAGGGTAAGCATCATGGCTGGC
AGCCTCACAGGTTTGCTTCTACTTCAGGCAGTGTCTGGGCATCAGGT
GCCCCCCCCCTGCATCCCTAAAAGCTTCGGCTACAGCTCGGTGGTGTGT
GTCTGCAATGCCACATACTGTGACTCCTTTGACCCCCGACCTTTCCT
GCCCTTGGTACCTTCAGCCGCTATGAGAGTACACGCAGTGGGCGACG
GATGGAGCTGAGTATGGGGCCCCATCCAGGCTAATCACACGGGCACAG
GCCTGCTACTGACCCTGCAGCCAGAACAGAAAGTCCAGAAAGTGAAG
GGATTGGAGGGGCCATGACAGATGCTGCTGCTCTCAACATCCTTGCC
CTGTCACCCCTGCCCAAATTTGCTACTTAAATCGTACTTCTCTGAA
GAAGGAATCGGATATAACATCATCCGGGTACCCATGGCCAGCTGTGA
CTTCTCCATCCGCACCTACACCTATGCAGACACCCCTGATGATTTCGA
GTTGCACAACCTCAGCCTCCAGAGGAAGATACCAAGCTCAAGATAC
CCCTGATTACCGAGCCCTGCAGTTGGCCAGCGTCCCGTTTCACTCC
TTGCCAGCCCCTGGACATCACCCACTTGGCTCAAGACCAATGGAGCG
GTGAATGGGAAGGGGTCACTCAAGGGACAGCCCGGAGACATCTACC
ACCAGACCTGGGCCAGATACTTTGTGAAGTTCTGGATGCCTATGCTG
AGCACAAAGTTACAGTTCTGGGCAGTGACAGCTGAAATGAGCCTTCT
GCTGGGCTGTTGAGTGGATACCCCTTCCAGTGCCTGGGCTTCACCCT
GAACATCAGCGAGACTTCATTGCCCCTGACCTAGTCTACCTCGCC
AACAGTACTCACCACAAATGTCGCCCTACTCATGCTGGATGACCAACGC
TTGCTGCTGCCCCACTGGGCAAAGGTGGTACTGACAGACCCAGAAGC
AGCTAAATATGTTTCATGGCATTGCTGTACATTGGTACTGGACTTCT
GGCTCCAGCCAAAGCCACCCTAGGGGAGACACACCGCCTGTTCCCCA
ACACCATGCTCTTTGCCTCAGAGGCCTGTGTGGGCTCCAAGTTCTGGG
AGCAGAGTGTGCGGCTAGGCTCCTGGGATCGAGGGATGCAGTACAGC
CACAGCATCATCAGAACCTCCTGTACCATGTGTGTCGGCTGGACCGAC
TGGAACCTTGCCCTGAACCCCGAAGGAGGACCCAATTGGGTGCGTAA
CTTTGTCGACAGTCCCATCATTGTAGACATCACCAAGGACACGTTTA
CAAAACAGCCCATGTTCTACCACCTTGGCCAGCTCAGCAAGTTCATTCC
TGAGGGCTCCCAGAGAGTGGGGCTGGTTGCCAGTCAGAAGAACGACC
TGGACGCAGTGGCACTGATGCATCCCGATGGCTCTGCTGTTGTGGTCTG
TGCTAAACCGCTCCTCTAAGGATGTGCCTCTTACCATCAAGGATCCTG
CTGTGGGCTTCTTGAGACAATCTCACCTGGCTACTCCATTACACCT
ACCTGTGGCATCGCCAGTATGGAGCAGATACTCAAGGAGGCATGG
GCTCAGCCTGGGCATTAAAGGGACAGAGTCAAGTCAACACGCTGTCTG
TGACTAAAGAGGGCACAGCAGGGCCAGTGTGAGCTTACAGCGACGT

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FIG. 62A-2

AAGCCCAGGGGCAATGGTTTGGGTGACTCACTTTCCCCTCTAGGTGGT
 GCCCAGGGCTGGAGGCCCTAGAAAAAGATCAGTAAGCCCCAGTGTC
 CCCCCAGCCCCCATGCTTATGTGAACATGCGCTGTGTGCTGCTTGCTT
 TGGAAACT

FIG. 62B

Met Glu Phe Ser Ser Pro Ser Arg Glu Glu Cys Pro Lys Pro Leu Ser Arg Val Ser
 Ile Met Ala Gly Ser Leu Thr Gly Leu Leu Leu Leu Gln Ala Val Ser Trp Ala Ser
 Gly Ala Arg Pro Cys Ile Pro Lys Ser Phe Gly Tyr Ser Ser Val Val Cys Val Cys
 Asn Ala Thr Tyr Cys Asp Ser Phe Asp Pro Pro Thr Phe Pro Ala Leu Gly Thr
 Phe Ser Arg Tyr Glu Ser Thr Arg Ser Gly Arg Arg Met Glu Leu Ser Met Gly
 Pro Ile Gln Ala Asn His Thr Gly Thr Gly Leu Leu Leu Thr Leu Gln Pro Glu Gln
 Lys Phe Gln Lys Val Lys Gly Phe Gly Gly Ala Met Thr Asp Ala Ala Ala Leu
 Asn Ile Leu Ala Leu Ser Pro Pro Ala Gln Asn Leu Leu Lys Ser Tyr Phe Ser
 Glu Glu Gly Ile Gly Tyr Asn Ile Ile Arg Val Pro Met Ala Ser Cys Asp Phe Ser
 Ile Arg Thr Tyr Thr Tyr Ala Asp Thr Pro Asp Asp Phe Gln Leu His Asn Phe Ser
 Leu Pro Glu Glu Asp Thr Lys Leu Lys Ile Pro Leu Ile His Arg Ala Leu Gln Leu
 Ala Gln Arg Pro Val Ser Leu Leu Ala Ser Pro Trp Thr Ser Pro Thr Trp Leu Lys
 Thr Asn Gly Ala Val Asn Gly Lys Gly Ser Leu Lys Gly Gln Pro Gly Asp Ile
 Tyr His Gln Thr Trp Ala Arg Tyr Phe Val Lys Phe Leu Asp Ala Tyr Ala Glu
 His Lys Leu Gln Phe Trp Ala Val Thr Ala Glu Asn Glu Pro Ser Ala Gly Leu
 Leu Ser Gly Tyr Pro Phe Gln Cys Leu Gly Phe Thr Pro Glu His Gln Arg Asp
 Phe Ile Ala Arg Asp Leu Gly Pro Thr Leu Ala Asn Ser Thr His His Asn Val Arg
 Leu Leu Met Leu Asp Asp Gln Arg Leu Leu Leu Pro His Trp Ala Lys Val Val
 Leu Thr Asp Pro Glu Ala Ala Lys Tyr Val His Gly Ile Ala Val His Trp Tyr Leu
 Asp Phe Leu Ala Pro Ala Lys Ala Thr Leu Gly Glu Thr His Arg Leu Phe Pro
 Asn Thr Met Leu Phe Ala Ser Glu Ala Cys Val Gly Ser Lys Phe Trp Glu Gln Ser
 Val Arg Leu Gly Ser Trp Asp Arg Gly Met Gln Tyr Ser His Ser Ile Ile Thr Asn
 Leu Leu Tyr His Val Val Gly Trp Thr Asp Trp Asn Leu Ala Leu Asn Pro Glu
 Gly Gly Pro Asn Trp Val Arg Asn Phe Val Asp Ser Pro Ile Ile Val Asp Ile Thr
 Lys Asp Thr Phe Tyr Lys Gln Pro Met Phe Tyr His Leu Gly His Phe Ser Lys
 Phe Ile Pro Glu Gly Ser Gln Arg Val Gly Leu Val Ala Ser Gln Lys Asn Asp Leu
 Asp Ala Val Ala Leu Met His Pro Asp Gly Ser Ala Val Val Val Val Leu Asn
 Arg Ser Ser Lys Asp Val Pro Leu Thr Ile Lys Asp Pro Ala Val Gly Phe Leu Glu
 Thr Ile Ser Pro Gly Tyr Ser Ile His Thr Tyr Leu Trp His Arg Gln

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FIG. 63A

ATGGATGCAATGAAGAGAGGGCTCTGCTGTGTGCTGCTGCTGTGTGG
AGCAGTCTTCGTTTCGCCCAGCCAGGAAATCCATGCCCGATTTCAGAA
GAGGAGCCAGATCTTACCAAGTGATCTGCAGAGATGAAAAAACGCA
GATGATATACCAGCAACATCAGTCATGGCTGCGCCCTGTGCTCAGAA
GCAACCGGGTGGAATATTGCTGGTGC AACAGTGGCAGGGCACAGTGC
CACTCAGTGCCTGTCAAAAGTTGCAGCGAGCCAAGGTGTTTCAACGG
GGGCACCTGCCAGCAGGCCCTGTACTTCTCAGATTTTCGTGTGCCAGTG
CCCCGAAGGATTTGCTGGGAAGTGCTGTGAAATAGATACCAGGGCCA
CGTGCTACGAGGACCAGGGCATCAGCTACAGGGGACAGTGGAGCAC
AGCGGAGAGTGGCGCCGAGTGCACCAACTGGAACAGCAGCGCGTTG
GCCCAGAAAGCCCTACAGCGGGCGGAGGCCAGACGCCATCAGGCTGG
GCCTGGGGAACCACAACCTACTGCAGAAACCCAGATCGAGACTCAAA
GCCCTGGTGCTACGTCTTTAAGGCGGGGAAGTACAGCTCAGAGTTCT
GCAGCACCCCTGCGCTCTCTGAGGGAAACAGTGACTGCTACTTTGGG
AATGGGTCAGCCTACCGTGGCACGCACAGCCTCACCGAGTCGGGTGC
CTCCTGCCTCCCGTGGAATTCCATGATCCTGATAGGCAAGGTTTACAC
AGCACAGAACCCAGTGCCCAGGCACTGGGCCTGGGCAACATAATT
ACTGCCGGAATCCTGATGGGGATGCCAAGCCCTGGTGCCACGTGCTG
AAGAACCGCAGGCTGACGTGGGAGTACTGTGATGTGCCCCTCTGCTC
CACCTGCGGCCTGAGACAGTACAGCCAGCCTCAGTTTCGCATCAAAG
GAGGGCTCTTCGCGGACATCGCCTCCACCCCTGGCAGGCTGCCATCT
TTGCCAAGCACAGGAGGTGCGCGGGAGAGCGGTTCTGTGCGGGGGC
ATACTCATCAGTCTCTGCTGGATTCTCTCTGCCGCCCACTGCTTCCAG
GAGAGGTTTCCGCCCCACCACCTGACGGTGATCTTGGGCAGAACATA
CCGGTGGTCCCTGGCGAGGAGGAGCAGAAATTGAAAGTCGAAAAA
TACATTGTCCATAAGGAATTCGATGATGACACTTACGACAATGACAT
TGCGCTGCTGCAGCTGAAATCGGATTTCGTCCCCTGTGCCAGGAGA
GCAGCGTGGTCCGCACTGTGTGCCTTCCCCCGCGGACCTGCAGCTG
CCGGA CTGGACGGAGTGTGAGCTCTCCGGCTACGGCAAGCATGAGGC
CTTGCTCTCTTTCTATTTCGGAGCGGCTGAAGGAGGCTCATGTGAGCT
GTACCCATCCAGCCGCTGCACATCACAACATTTACTTAACAGAACAG
TCACCGACAACATGCTGTGTGCTGGAGACACTCGGAGCGGCGGGCCC
CAGGCAAACTTGACGACGCCTGCCAGGGCGATTTCGGAGGCCCCCT
GGTGTGTCTGAACGATGGCCGCATGACTTTGGTGGGCATCATCAGCT
GGGGCCTGGGCTGTGGACAGAAGGATGTCCCGGGTGTGTACACCAAG
GTTACCAACTACCTAGACTGGATTTCGTGACAACATGCGACCGTGACC
AGGAACACCCGACTCCTCAAAAGCAAATGAGATCC

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FIG. 63B

Met Asp Ala Met Lys Arg Gly Leu Cys Cys Val Leu Leu Leu Cys Gly Ala Val
Phe Val Ser Pro Ser Gln Glu Ile His Ala Arg Phe Arg Arg Gly Ala Arg Ser Tyr
Gln Val Ile Cys Arg Asp Glu Lys Thr Gln Met Ile Tyr Gln Gln His Gln Ser Trp
Leu Arg Pro Val Leu Arg Ser Asn Arg Val Glu Tyr Cys Trp Cys Asn Ser Gly
Arg Ala Gln Cys His Ser Val Pro Val Lys Ser Cys Ser Glu Pro Arg Cys Phe Asn
Gly Gly Thr Cys Gln Gln Ala Leu Tyr Phe Ser Asp Phe Val Cys Gln Cys Pro
Glu Gly Phe Ala Gly Lys Cys Cys Glu Ile Asp Thr Arg Ala Thr Cys Tyr Glu
Asp Gln Gly Ile Ser Tyr Arg Gly Thr Trp Ser Thr Ala Glu Ser Gly Ala Glu Cys
Thr Asn Trp Asn Ser Ser Ala Leu Ala Gln Lys Pro Tyr Ser Gly Arg Arg Pro Asp
Ala Ile Arg Leu Gly Leu Gly Asn His Asn Tyr Cys Arg Asn Pro Asp Arg Asp
Ser Lys Pro Trp Cys Tyr Val Phe Lys Ala Gly Lys Tyr Ser Ser Glu Phe Cys Ser
Thr Pro Ala Cys Ser Glu Gly Asn Ser Asp Cys Tyr Phe Gly Asn Gly Ser Ala Tyr
Arg Gly Thr His Ser Leu Thr Glu Ser Gly Ala Ser Cys Leu Pro Trp Asn Ser Met
Ile Leu Ile Gly Lys Val Tyr Thr Ala Gln Asn Pro Ser Ala Gln Ala Leu Gly Leu
Gly Lys His Asn Tyr Cys Arg Asn Pro Asp Gly Asp Ala Lys Pro Trp Cys His
Val Leu Lys Asn Arg Arg Leu Thr Trp Glu Tyr Cys Asp Val Pro Ser Cys Ser
Thr Cys Gly Leu Arg Gln Tyr Ser Gln Pro Gln Phe Arg Ile Lys Gly Gly Leu Phe
Ala Asp Ile Ala Ser His Pro Trp Gln Ala Ala Ile Phe Ala Lys His Arg Arg Ser
Pro Gly Glu Arg Phe Leu Cys Gly Gly Ile Leu Ile Ser Ser Cys Trp Ile Leu Ser
Ala Ala His Cys Phe Gln Glu Arg Phe Pro Pro His His Leu Thr Val Ile Leu Gly
Arg Thr Tyr Arg Val Val Pro Gly Glu Glu Glu Gln Lys Phe Glu Val Glu Lys
Tyr Ile Val His Lys Glu Phe Asp Asp Asp Thr Tyr Asp Asn Asp Ile Ala Leu
Leu Gln Leu Lys Ser Asp Ser Ser Arg Cys Ala Gln Glu Ser Ser Val Val Arg
Thr Val Cys Leu Pro Pro Ala Asp Leu Gln Leu Pro Asp Trp Thr Glu Cys Glu
Leu Ser Gly Tyr Gly Lys His Glu Ala Leu Ser Pro Phe Tyr Ser Glu Arg Leu Lys
Glu Ala His Val Arg Leu Tyr Pro Ser Ser Arg Cys Thr Ser Gln His Leu Leu Asn
Arg Thr Val Thr Asp Asn Met Leu Cys Ala Gly Asp Thr Arg Ser Gly Gly Pro
Gln Ala Asn Leu His Asp Ala Cys Gln Gly Asp Ser Gly Gly Pro Leu Val Cys
Leu Asn Asp Gly Arg Met Thr Leu Val Gly Ile Ser Trp Gly Leu Gly Cys Gly
Gln Lys Asp Val Pro Gly Val Tyr Thr Lys Val Thr Asn Tyr Leu Asp Trp Ile Arg
Asp Asn Met

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FIG. 64A

ATCACTCTCTTTAATCACTACTCACATTAACCTCAACTCCTGCCACAA
TGTACAGGATGCAACTCCTGTCTTGCAATTGCACTAATCTTGCACTTG
TCACAAACAGTGCACCTACTTCAAGTTCGACAAAAGAAAAACAAAGAAA
ACACAGCTACAACCTGGAGCATTTACTGCTGGATTTACAGATGATTTTG
AATGGAATTAATAATTACAAGAATCCCAAACCTCACCAGGATGCTCAC
ATTTAAGTTTTACATGCCCAAGAAGGCCACAGAACTGAAACAGCTTC
AGTGTCTAGAAGAAGAACTCAAACCTCTGGAGGAAGTGCTGAATTTA
GCTCAAAGCAAAAACTTTCACTTAAGACCCAGGGACTTAATCAGCAA
TATCAACGTAATAGTTCTGGAACATAAGGGATCTGAAACAACATTC
TGTGTGAATATGCAGATGAGACAGCAACCATGTAGAATTTCTGAAC
AGATGGATTACCTTTTGTCAAAGCATCATCTCAACACTAACTTGATAA
TTAAGTGCTTCCCACCTAAAACATATCAGGCCTTCTATTATTTATTTA
AATATTTAAATTTTATATTTATTGTTGAATGTATGGTTGCTACCTATTG
TAACTATTATCTTAATCTTAAAACTATAAATATGGATCTTTATGAT
TCTTTTGTAAAGCCCTAGGGGCTCTAAAAATGGTTTACCTTATTTATCC
CAAAAATATTTTATTATTATGTGAATGTTAAATATAGTATCTATGTAG
ATTGGTTAGTAAACTATTTAATAAATTTGATAAATATAAAAAAAAAA
AAACAAAAAAAAAAAA

FIG. 64B

Met Tyr Arg Met Gln Leu Leu Ser Cys Ile Ala Leu Ile Leu Ala Leu Val Thr Asn
Ser Ala Pro Thr Ser Ser Ser Thr Lys Lys Thr Lys Lys Thr Gln Leu Gln Leu Glu
His Leu Leu Leu Asp Leu Gln Met Ile Leu Asn Gly Ile Asn Asn Tyr Lys Asn
Pro Lys Leu Thr Arg Met Leu Thr Phe Lys Phe Tyr Met Pro Lys Lys Ala Thr
Glu Leu Lys Gln Leu Gln Cys Leu Glu Glu Glu Leu Lys Pro Leu Glu Glu Val
Leu Asn Leu Ala Gln Ser Lys Asn Phe His Leu Arg Pro Arg Asp Leu Ile Ser
Asn Ile Asn Val Ile Val Leu Glu Leu Lys Gly Ser Glu Thr Thr Phe Met Cys Glu
Tyr Ala Asp Glu Thr Ala Thr Ile Val Glu Phe Leu Asn Arg Trp Ile Thr Phe Cys
Gln Ser Ile Ile Ser Thr Leu Thr

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FIG. 65A-1

ATGCAAATAGAGCTCTCCACCTGCTTCTTTCTGTGCCTTTTGCGATTCT
GCTTTAGTGGCACCAGAAGATACTACCTGGGTGCAGTGGAACTGTCA
TGGGACTATATGCAAAAGTGATCTCGGTGAGCTGCCTGTGGACGCAAG
ATTTCTCTCTAGAGTGCCAAAATCTTTTCCATTCAACACCTCAGTCGT
GTACAAAAAGACTCTGTTTGTAGAATTCACGGATCACCTTTTCAACAT
CGCTAAGCCAAAGGCCACCCTGGATGGGTCTGCTAGGTCTACCATCC
AGGCTGAGGTTTATGATACAGTGGTCATTACACTTAAGAACATGGCT
TCCCATCCTGTGAGTCTTCATGCTGTTGGTGTATCCTACTGGAAAGCT
TCTGAGGGAGCTGAATATGATGATCAGACCAGTCAAAGGGAGAAAG
AAGATGATAAAGTCTTCCCTGGTGGAAAGCCATACATATGTCTGGCAG
GTCCTGAAAGAGAAATGGTCCAATGGCCTCTGACCCACTGTGCCTTAC
CTACTCATATCTTTCTCATGTGGACCTGGTAAAAGACTTGAATTCAGG
CCTCATTGGAGCCCTACTAGTATGTAGAGAAAGGAGTCTGGCCAAAGG
AAAAGACACAGACCTTGCACAAATTTATACTACTTTTGCTGTATTGT
ATGAAGGGAAAAGTTGGCACTCAGAAACAAAGAACTCCTTGATGCA
GGATAGGGATGCTGCATCTGCTCGGGCCTGGCCATAAAATGCACACAG
TCAATGGTTATGTAACAGGTCTCTGCCAGGTCTGATTGGATGCCACA
GGAAATCAGTCTATTGGCATGTGATTGGAATGGGACCCACTCCTGAA
GTGCACTCAATATTCTCGAAGGTACACATTTCTTGTGAGGAACCAT
CGCCAGGCGTCTTGGAAATCTCGCCAATAAATTTCTTACTGCTCAA
ACACTCTTGATGGACCTTGGACAGTTTCTACTGTTTGTCAATCTCTT
CCCACCAACATGATGGCATGGAAGCTTATGTCAAAAGTACAGACTGT
CCAGAGGAACCCCAACTACGAATGAAAAATAATGAAGAAGCGGAAG
ACTATGATGATGATCTTACTGATTCTGAAATGGATGTGGTCAGGTTTG
ATGATGACAACTCTCCTTCTTTATCCAAATTCGCTCAGTTGCCAAGA
AGCATCCTAAAACCTTGGGTACATTACATTGCTGCTGAAGAGGAGGAC
TGGGACTATGCTCCCTTAGTCTCGCCCCGATGACAGAAAGTTATAAA
AGTCAATATTTGAACAATGGCCCTCAGCGGATTGGTAGGAAGTACAA
AAAAGTCCGATTTATGGCATACACAGATGAAACCTTAAAGACTCGTG
AAGCTATTACAGCATGAATCAGGAATCTTGGGACCTTTACTTTATGGGG
AAGTTGGAGACACACTGTTGATTATTTAAGAATCAAGCAAGCAGA
CCATATAACATCTACCCCTACGGAATCACTGATGTCCGCTCTTTGTAT
TCAAGGAGATTACCAAAAAGGTGTAACACATTTGAAGGATTTTCCAAT
TCTGCCAGGAGAAATATTCAAATATAAATGGACAGTGAAGTGTAGAAG
ATGGGCCAACTAAATCAGATCCTCGGTGCCTGACCCGCTATTACTCTA
GTTTCGTTAATATGGAGAGAGATCTAGCTTCAGGACTCATTTGGCCCT
TCTCTACTGCTCTACAAAGAATCTGTAGATCAAAGAGGAAACCAGATA
ATGTCAGACAAGAGGAATGTCATCCTGTTTTCTGTATTTGATGAGAAC
CGAAGCTGGTACCTCACAGAGAATATACAACGCTTTCTCCCAATCCA
GCTGGAGTGCAGCTTGAGGATCCAGAGTTCCAAGCCTCCAACATCAT
GCACAGCATCAATGGCTATGTTTTGTAGTTTGTGATTTGTCAGTTTG
TTTGCATGAGGTGGCATACTGGTACATTCTAAGCATTGGAGCACAGA
CTGACTTCCTTTCTGTCTTCTTCTGATATACCTTCAAACACAAAAAT

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FIG. 65A-2

GGTCTATGAAGACACACTCACCTATTCCCATTCTCAGGAGAAAAGTGT
CTTCATGTGCGATGGAAAAACCCAGGTCTATGGATTCTGGGGTGCCACA
ACTCAGACTTTCGGAACAGAGGCATGACCGCCTTACTGAAGGTTTCT
AGTTGTGACAAGAACACTGGTGATTATTACGAGGACAGTTATGAAGA
TATTTTCAGCATACTTGCTGAGTAAAAACAATGCCATTGAACCAAGAA
GCTTCTCCCGAATTCAAGACACCGTAGCACTAGGCAAAAGCAATTT
AATGCCACCACAATTCCAGAAAAATGACATAGAGAAGACTGACCCTTG
GTTTGCACACAGAACACCTATGCCCTAAAATACAAAATGTCTCCTCTA
GTGATTTGTTGATGCTCTTGCGACAGAGTCCTACTCCACATGGGCTAT
CCTTATCTGATCTCCAAGAAGCCAAATATGAGACTTTTTCTGATGATC
CATCACCTGGAGCAATAGACAGTAATAACAGCCTGTCTGAAATGACA
CACTTCAGGCCACAGCTCCATCACAGTGGGGACATGGTATTTACCCC
TGAGTCAGGCCCTCCAATTAAAGATTAAATGAGAACTGGGGGAACTG
CAGCAACAGAGTTGAAGAACTTGATTTCAAAGTTTCTAGTACATCA
AATAATCTGATTTCAACAATCCATCAGACAATTTGGCAGCAGGTACT
GATAATACAAAGTTCTTAGGACCCCCAAGTATGCCAGTTCATTATGAT
AGTCAATTAGATACCACTCTATTTGGCAAAAAGTCATCTCCCCTTACT
GAGTCTGGTGGACCTCTGAGCTTGAGTGAAGAAAATATGATCAAA
GTTGTTAGAATCAAGTTTAAATGAATAGCCAAGAAAGTTTCATGGGGAA
AAAAATGTATCGTCAACAGAGAGTGGTAGGTTATTTAAAGGGAAAAAGA
GCTCATGGACCTGCTTTGTTGACTAAAGATAATGCCTTATTCAAAGTT
AGCATCTCTTTGTTAAAGACAAACAAAACCTTCCAATAATTCAGCAACT
AATAGAAAAGACTCACATTGATGGCCCATCATTATTAATTGAGAATAG
TCCATCAGTCTGGCAAAATATATTAGAAAAGTGACACTGAGTTTAAAA
AAGTGACACCTTTGATTTCATGACAGAAATGCTTATGGACAAAAATGCT
ACAGCTTTGAGGCTAAATCATATGTCAAATAAAACTACTTCATCAAA
AAACATGGAAATGGTCCAACAGAAAAAAGAGGGCCCCATTCCACCA
GATGCACAAAATCCAGATATGTGCTTCTTTAAGATGCTATTCTTGCCA
GAATCAGCAAGGTGGATACAAAGGACTCATGGAAAGAACTCTCTGAA
CTCTGGGCAAGGCCCCAGTCCAAAGCAATTAGTATCTTAGGACCCAG
AAAAATCTGTGGAGGTCAGAAATTTCTGTCTGAGAAAAACAAAGTG
GTAGTAGGAAAGGGTGAATTTACAAAGGACGTAGGACTCAAAGAGA
TGGTTTTTCCAAGCAGCAGAAAACCTATTTCTTACTAACTTGGATAATT
TACATGAAAAATAATACACACAATCAAGAAAAAAAATTCAGGAAGA
AATAGAAAAGAAGGAAACATTAATCCAAGAGAATGTAGTTTGCCTC
AGATACATACAGTGAAGTGGCACTAAGAATTTCAATGAAGAACCTTTTC
TTACTGAGCACTTAGGCAAAATGTAGAAGGTTTCATATGACGGGGCATA
TGCTCCAGTACTTCAAGATTTTAGGTCATTAATGATTCAACAAATAG
AACAAAGAAACACACAGCTCATTTCTCAAAAAAAGGGGAGGAAGAA
AACTTGGAAGGCTTGGGAAATCAAACCAGCAAAATGTAGAGAAATAT
GCATGCACCACAAGGAATATCTCCTAATACAAGCCAGCAGAATTTTG
TCACGCAACGTAGTAAGAGAGCTTTGAAACAATTCAGACTCCCACTA

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FIG. 65A-3

GAAGAAACAGAACTTGAAAAAAGGATAATTGTGGATGACACCTCAAC
CCAGTGGTCCAAAAACATGAAACATTTGACCCCGAGCACCTCACAC
AGATAGACTACAATGAGAAGGAGAAAGGGGCCATTACTCAGTCTCCC
TTATCAGATTGCCTTACGAGGAGTCATAGCATCCCTCAAGCAAAATAGA
TCTCCATTACCCATTGCAAAGGTATCATCATTTCCATCTATTAGACCTTA
TATATCTGACCAGGGTCTTATTCGAAGACAACCTCTTCTCATCTTCCAG
CAGCATCTTATAGAAAGAAAGATTCTGGGGTCCAAGAAAGCAGTCAT
TTCTTACAAGGAGCCAAAAAATAACCTTTCTTTAGCCATTCTAACC
TTGGAGATGACTGGTGATCAAAGAGAGGTTGGCTCCCTGGGGACAAG
TGCCACAAATTGAGTCACATACAAGAAAGTTGAGAACACTGTTCTCCC
GAAACCAGACTTGCCCAAAACATCTGGCAAAGTTGAATTGCTTCCAA
AAGTTCACATTTATCAGAAGGACCTATTCCCTACGGAACTAGCAATG
GGTCTCCTGGCCATCTGGATCTCGTGGAAGGGAGCCTTCTTCAGGGAA
CAGAGGGAGCGATTAAAGTGAATGAAGCAAAACAGACCTGAAAAAGT
TCCCTTTCTGAGAGTAGCAACAGAAAGCTCTGCAAGACTCCCTCCAA
GCTATTGGATCCTCTTGCTTGGGATAACCACTATGGTACTCAGATACC
AAAAGAAGAGTGGAAATCCCAAGAGAAGTCACCAGAAAAAACAGCT
TTTAAGAAAAAGGATACCATTTTGTCCCTGAACGCTTGTGAAAGCAAT
CATGCAATAGCAGCAATAAATGAGGGACAAAATAAGCCCGAAATAG
AAGTCACCTGGGCAAAGCAAGGTAGGACTGAAAGGCTGTGCTCTCAA
AACCCACCAAGTCTTGAAACGCCATCAACGGGAAATAACTCGTACTAC
TCTTCAGTCAGATCAAGAGGAAATTGACTATGATGATACCATATCAGT
TGAAATGAAGAAGGAAGATTTTGACATTTATGATGAGGATGAAAAATC
AGAGCCCCCGACGCTTTCAAAGAAAAACACGACACTATTTTATTGCTG
CAGTGGAGAGGCTCTGGGATTATGGGATGAGTACGCTCCCAACATGTT
CTAAGAAACAGGGCTCAGAGTGGCAGTGTCCCTCAGTTCAAGAAAGT
TGTTTTCCAGGAATTTACTGATGGCTCCTTTACTCAGCCCTTATACCGT
GGAGAACTAAATGAACATTTGGGACTCCTGGGGCCATATATAAGAGC
AGAAGTTGAAGATAATATCATGGTAACTTTCAGAAATCAGGCCTCTC
GTCCTATTCTCTTATCTAGCCTTATTTCTTATGAGGAAGATCAGAG
GCAAGGAGCAGAACCTAGAAAAAACTTTGTCAAGCCTAATGAAACCA
AAACTTACTTTTGAAAAGTGCAACATCATATGGCACCCACTAAAGAT
GAGTTTGACTGCAAAGCCTGGGCTTATTTCTCTGATGTTGACCTGGAA
AAAGATGTGCACTCAGGCCTGATTGGACCCCTCTGGCTGCCACACT
AACACACTGAACCCCTGCTCATGGGAGACAAGTGACAGTACAGGAATT
TGCTCTGTTTTTACCACATCTTTGATGAGACCAAAAGCTGGTACTTCACT
GAAAATATGGAAAGAAACTGCAGGGCTCCCTGCAATATCCAGATGGA
AGATCCCCTTTTAAAGAGAATTATCGCTTCCATGCAATCAATGGCTA
CATAATGGATACACTACCTGGCTTAGTAATGGCTCAGGATCAAAGGA
TTCGATGGTATCTGCTCAGCATGGGCAGCAATGAAAAACATCCATTCT
ATTCATTTCACTGGACATGTGTTCACTGTACGAAAAAAGAGGAGTA
TAAATGGCACTGTACAATCTCTATCCAGGTGTTTTTGAGACAGTGGAA

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FIG. 65A-4

AATGTTACCATCCAAAGCTGGAATTTGGCGGGTGAATGCCTTATTGG
CGAGCATCTACATGCTGGGATGAGCACACTTTTTCTGGTGTACAGCAA
TAAGTGTACAGACTCCCCTGGGAATGGCTTCTGGACACATTAGAGATTT
TCAGATTACAGCTTTCAGGACAATATGGACAGTGGGCCCCAAAGCTGG
CCAGACTTCATTATTCCGGATCAATCAATGCCTGGAGCACCAGGAG
CCCTTTTCTTGGATCAAGGTGGATCTGTTGGCACCAATGATTATTCAC
GGCATCAAGACCCAGGGTGCCCGTCAGAAGTTCTCCAGCCTCTACAT
CTCTCAGTTTATCATCATGTATAGTCTTGATGGGAAGAAGTGGCAGA
CTTATCGAGGAAATTCCTACTGGAACCTTAATGGTCTTCTTGGCAATG
TGGATTTCATCTGGGATAAAAACACAATATTTTAAACCCCTCAATTATTG
CTCGATACATCCGTTTGCACCCACTCATTATAGCATTTCGCAGCACTC
TTCGCATGGAGTTGATGGGCTGTGATTTAAATAGTTGCAGCATGCCAT
TGGGAATGGAGAGTAAAGCAATATCAGATGCACAGATTACTGCTTCA
TCCTACTTTACCAATATGTTTGCCACCTGGTCTCCTTCAAAGCTCGA
CTTCACCTCCAAGGGAGGAGTAATGCCTGGAGACCTCAGGTGAATAA
TCCAAAAGAGTGGCTGCAAGTGGACTTCCAGAAGACAATGAAAGTCA
CAGGAGTAACCTACTCAGGGAGTAAATCTCTGCTTACCAGCATGTAT
GTGAAGGAGTTCCTCATCTCCAGCAGTCAAGATGGCCATCAGTGGAC
TCTCTTTTTTCAGAATGGCAAAGTAAAGGTTTTTCAGGGAAATCAAGA
CTCCTTCACACCTGTGGTGAACCTCTAGACCCACCGTTACTGACTCG
CTACCTTCGAATTCACCCCCAGAGTTGGGTGCACCAAGATTGCCGTGAG
GATGGAGGTTCTGGGCTGCGAGGCACAGGACCTCTACTGAGGGTGGC
CACTGCAGCACTGCCACTGCGCGTCACCTCTCCCTCCTCAGCTCCAGG
GCAGTGTCCCTCCCTGGCTTGCCTTCTACCTTTGTGCTAAATCCTAGC
AGACACTGCCTTGAAGCCTCCTGAATTAACATATCATCAGTCTGCATT
TCTTTGGTGGGGGGCCAGGAGGGTGCATCCAATTTAACTTAACCTTA
CCTATTTTCTGCAGCTGCTCCAGATTACTCCTTCCTTCCAATATAACT
AGGCAAAAAGAAGTGAGGAGAAACCTGCATGAAAGCATTTCTCCCTG
AAAAGTTAGCCCTCTCAGAGTCACCACCTTCTCTGTTGTAGAAAACT
ATGTGATGAAACTTTGAAAAAGATATTTATGATGTTAACATTTCAAGT
TAAGCCTCATACGTTTAAAAATAAACTCTCAGTTGTTTATTATCCTGA
TCAAGCATGGAACAAAGCATGTTTCAGGATCAGATCAATACAATCTT
GGAGTCAAAAGGCAAATCATTGGACAATCTGCAAAATGGAGAGAA
TACAATAACTACTACAGTAAAGTCTGTTCTGCTTCTTACACATAGA
TATAATTATGTTATTTAGTCATTATGAGGGGCACATTCTTATCTCCAA
AACTAGCATTTCTTAACTGAGAATTATAGATGGGGTTCAAGAATCCC
TAAGTCCCTGAAATTATATAAGGCATTCTGTATAAATGCAAATGTGC
ATTTTTCTGACGAGTGTCCATAGATATAAAGCCATTTGGTCTTAATTCT
GACCAATAAAAAAATAAGTCAGGAGGATGCAATTGTTGAAAGCTTTG
AAATAAAATAACAATGTCTTCTTGAATTTGTGATGGCCAAGAAAGA
AAATGATGA

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FIG. 65B-1

Met Gln Ile Glu Leu Ser Thr Cys Phe Phe Leu Cys Leu Leu Arg Phe Cys Phe Ser
 Ala Thr Arg Arg Tyr Tyr Leu Gly Ala Val Glu Leu Ser Trp Asp Tyr Met Gln Ser
 Asp Leu Gly Glu Leu Pro Val Asp Ala Arg Phe Pro Pro Arg Val Pro Lys Ser Phe
 Pro Phe Asn Thr Ser Val Val Tyr Lys Lys Thr Leu Phe Val Glu Phe Thr Asp His
 Leu Phe Asn Ile Ala Lys Pro Arg Pro Pro Trp Met Gly Leu Leu Gly Pro Thr Ile
 Gln Ala Glu Val Tyr Asp Thr Val Val Ile Thr Leu Lys Asn Met Ala Ser His Pro
 Val Ser Leu His Ala Val Gly Val Ser Tyr Trp Lys Ala Ser Glu Gly Ala Glu Tyr
 Asp Asp Gln Thr Ser Gln Arg Glu Lys Glu Asp Asp Lys Val Phe Pro Gly Gly
 Ser His Thr Tyr Val Trp Gln Val Leu Lys Glu Asn Gly Pro Met Ala Ser Asp Pro
 Leu Cys Leu Thr Tyr Ser Tyr Leu Ser His Val Asp Leu Val Lys Asp Leu Asn
 Ser Gly Leu Ile Gly Ala Leu Leu Val Cys Arg Glu Gly Ser Leu Ala Lys Glu Lys
 Thr Gln Thr Leu His Lys Phe Ile Leu Leu Phe Ala Val Phe Asp Glu Gly Lys Ser
 Trp His Ser Glu Thr Lys Asn Ser Leu Met Gln Asp Arg Asp Ala Ala Ser Ala Arg
 Ala Trp Pro Lys Met His Thr Val Asn Gly Tyr Val Asn Arg Ser Leu Pro Gly Leu
 Ile Gly Cys His Arg Lys Ser Val Tyr Trp His Val Ile Gly Met Gly Thr Thr Pro
 Glu Val His Ser Ile Phe Leu Glu Gly His Thr Phe Leu Val Arg Asn His Arg Gln
 Ala Ser Leu Glu Ile Ser Pro Ile Thr Phe Leu Thr Ala Gln Thr Leu Leu Met Asp
 Leu Gly Gln Phe Leu Leu Phe Cys His Ile Ser Ser His Gln His Asp Gly Met Glu
 Ala Tyr Val Lys Val Asp Ser Cys Pro Glu Glu Pro Gln Leu Arg Met Lys Asn
 Asn Glu Glu Ala Glu Asp Tyr Asp Asp Asp Leu Thr Asp Ser Glu Met Asp Val
 Val Arg Phe Asp Asp Asp Asn Ser Pro Ser Phe Ile Gln Ile Arg Ser Val Ala Lys
 Lys His Pro Lys Thr Trp Val His Tyr Ile Ala Ala Glu Glu Glu Asp Trp Asp Tyr
 Ala Pro Leu Val Leu Ala Pro Asp Asp Arg Ser Tyr Lys Ser Gln Tyr Leu Asn
 Asn Gly Pro Gln Arg Ile Gly Arg Lys Tyr Lys Lys Val Arg Phe Met Ala Tyr Thr
 Asp Glu Thr Phe Lys Thr Arg Glu Ala Ile Gln His Glu Ser Gly Ile Leu Gly Pro
 Leu Leu Tyr Gly Glu Val Gly Asp Thr Leu Leu Ile Ile Phe Lys Asn Gln Ala Ser
 Arg Pro Tyr Asn Ile Tyr Pro His Gly Ile Thr Asp Val Arg Pro Leu Tyr Ser Arg
 Arg Leu Pro Lys Gly Val Lys His Leu Lys Asp Phe Pro Ile Leu Pro Gly Glu Ile
 Phe Lys Tyr Lys Trp Thr Val Thr Val Glu Asp Gly Pro Thr Lys Ser Asp Pro Arg
 Cys Leu Thr Arg Tyr Tyr Ser Ser Phe Val Asn Met Glu Arg Asp Leu Ala Ser
 Gly Leu Ile Gly Pro Leu Leu Ile Cys Tyr Lys Glu Ser Val Asp Gln Arg Gly Asn
 Gln Ile Met Ser Asp Lys Arg Asn Val Ile Leu Phe Ser Val Phe Asp Glu Asn Arg
 Ser Trp Tyr Leu Thr Glu Asn Ile Gln Arg Phe Leu Pro Asn Pro Ala Gly Val Gln
 Leu Glu Asp Pro Glu Phe Gln Ala Ser Asn Ile Met His Ser Ile Asn Gly Tyr Val
 Phe Asp Ser Leu Gln Leu Ser Val Cys Leu His Glu Val Ala Tyr Trp Tyr Ile Leu
 Ser Ile Gly Ala Gln Thr Asp Phe Leu Ser Val Phe Phe Ser Gly Tyr Thr Phe Lys
 His Lys Met Val Tyr Glu Asp Thr Leu Thr Leu Phe Pro Phe Ser Gly Glu Thr Val
 Phe Met Ser Met Glu Asn Pro Gly Leu Trp Ile Leu Gly Cys His Asn Ser Asp Phe
 Arg Asn Arg Gly Met Thr Ala Leu Leu Lys Val Ser Ser Cys Asp Lys Asn Thr
 Gly Asp Tyr Tyr Glu Asp Ser Tyr Glu Asp Ile Ser Ala Tyr Leu Leu Ser Lys Asn
 Asn Ala Ile Glu Pro Arg Ser Phe Ser Gln Asn Ser Arg His Arg Ser Thr Arg Gln
 Lys Gln Phe Asn Ala Thr Thr Ile Pro Glu Asn Asp Ile Glu Lys Thr Asp Pro Trp

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FIG. 65B-2

Phe Ala His Arg Thr Pro Met Pro Lys Ile Gln Asn Val Ser Ser Ser Asp Leu Leu
 Met Leu Leu Arg Gln Ser Pro Thr Pro His Gly Leu Ser Leu Ser Asp Leu Gln Glu
 Ala Lys Tyr Glu Thr Phe Ser Asp Asp Pro Ser Pro Gly Ala Ile Asp Ser Asn Asn
 Ser Leu Ser Glu Met Thr His Phe Arg Pro Gln Leu His His Ser Gly Asp Met Val
 Phe Thr Pro Glu Ser Gly Leu Gln Leu Arg Leu Asn Glu Lys Leu Gly Thr Thr
 Ala Ala Thr Glu Leu Lys Lys Leu Asp Phe Lys Val Ser Ser Thr Ser Asn Asn Leu
 Ile Ser Thr Ile Pro Ser Asp Asn Leu Ala Ala Gly Thr Asp Asn Thr Ser Ser Leu
 Gly Pro Pro Ser Met Pro Val His Tyr Asp Ser Gln Leu Asp Thr Thr Leu Phe Gly
 Lys Lys Ser Ser Pro Leu Thr Glu Ser Gly Gly Pro Leu Ser Leu Ser Glu Glu Asn
 Asn Asp Ser Lys Leu Leu Glu Ser Gly Leu Met Asn Ser Gln Glu Ser Ser Trp Gly
 Lys Asn Val Ser Ser Thr Glu Ser Gly Arg Leu Phe Lys Gly Lys Arg Ala His Gly
 Pro Ala Leu Leu Thr Lys Asp Asn Ala Leu Phe Lys Val Ser Ile Ser Leu Leu
 Lys Thr Asn Lys Thr Ser Asn Asn Ser Ala Thr Asn Arg Lys Thr His Ile Asp
 Gly Pro Ser Leu Leu Ile Glu Asn Ser Pro Ser Val Trp Gln Asn Ile Leu Glu Ser
 Asp Thr Glu Phe Lys Lys Val Thr Pro Leu Ile His Asp Arg Met Leu Met Asp
 Lys Asn Ala Thr Ala Leu Arg Leu Asn His Met Ser Asn Lys Thr Thr Ser Ser
 Lys Asn Met Glu Met Val Gln Gln Lys Lys Glu Gly Pro Ile Pro Pro Asp Ala
 Gln Asn Pro Asp Met Ser Phe Phe Lys Met Leu Phe Leu Pro Glu Ser Ala Arg
 Trp Ile Gln Arg Thr His Gly Lys Asn Ser Leu Asn Ser Gly Gln Gly Pro Ser Pro
 Lys Gln Leu Val Ser Leu Gly Pro Glu Lys Ser Val Glu Gly Gln Asn Phe Leu
 Ser Glu Lys Asn Lys Val Val Val Gly Lys Gly Glu Phe Thr Lys Asp Val Gly
 Leu Lys Glu Met Val Phe Pro Ser Ser Arg Asn Leu Phe Leu Thr Asn Leu Asp
 Asn Leu His Glu Asn Asn Thr His Asn Gln Glu Lys Lys Ile Gln Glu Glu Ile
 Glu Lys Lys Glu Thr Leu Ile Gln Glu Asn Val Val Leu Pro Gln Ile His Thr
 Val Thr Gly Thr Lys Asn Phe Met Lys Asn Leu Phe Leu Leu Ser Thr Arg Gln
 Asn Val Glu Gly Ser Tyr Asp Gly Ala Tyr Ala Pro Val Leu Gln Asp Phe Arg
 Ser Leu Asn Asp Ser Thr Asn Arg Thr Lys Lys His Thr Ala His Phe Ser Lys
 Lys Gly Glu Glu Glu Asn Leu Glu Gly Leu Gly Asn Gln Thr Lys Gln Ile Val
 Glu Lys Tyr Ala Cys Thr Thr Arg Ile Ser Pro Asn Thr Ser Gln Gln Asn Phe
 Val Thr Gln Arg Ser Lys Arg Ala Leu Lys Gln Phe Arg Leu Pro Leu Glu Glu
 Thr Glu Leu Glu Lys Arg Ile Ile Val Asp Asp Thr Ser Thr Gln Trp Ser Lys Asn
 Met Lys His Leu Thr Pro Ser Thr Leu Thr Gln Ile Asp Tyr Asn Glu Lys Glu
 Lys Gly Ala Ile Thr Gln Ser Pro Leu Ser Asp Cys Leu Thr Arg Ser His Ser Ile
 Pro Gln Ala Asn Arg Ser Pro Leu Pro Ile Ala Lys Val Ser Ser Phe Pro Ser Ile
 Arg Pro Ile Tyr Leu Thr Arg Val Leu Phe Gln Asp Asn Ser Ser His Leu Pro
 Ala Ala Ser Tyr Arg Lys Lys Asp Ser Gly Val Gln Glu Ser Ser His Phe Leu
 Gln Gly Ala Lys Lys Asn Asn Leu Ser Leu Ala Ile Leu Thr Leu Glu Met Thr
 Gly Asp Gln Arg Glu Val Gly Ser Leu Gly Thr Ser Ala Thr Asn Ser Val Thr
 Tyr Lys Lys Val Glu Asn Thr Val Leu Pro Lys Pro Asp Leu Pro Lys Thr Ser
 Gly Lys Val Glu Leu Leu Pro Lys Val His Ile Tyr Gln Lys Asp Leu Phe Pro
 Thr Glu Thr Ser Asn Gly Ser Pro Gly His Leu Asp Leu Val Glu Gly Ser Leu

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FIG. 65B-3

Leu Gln Gly Thr Glu Gly Ala Ile Lys Trp Asn Glu Ala Asn Arg Pro Gly Lys
 Val Pro Phe Leu Arg Val Ala Thr Glu Ser Ser Ala Lys Thr Pro Ser Lys Leu
 Leu Asp Pro Leu Ala Trp Asp Asn His Tyr Gly Thr Gln Ile Pro Lys Glu Glu
 Trp Lys Ser Gln Glu Lys Ser Pro Glu Lys Thr Ala Phe Lys Lys Lys Asp Thr Ile
 Leu Ser Leu Asn Ala Cys Glu Ser Asn His Ala Ile Ala Ala Ile Asn Glu Gly
 Gln Asn Lys Pro Glu Ile Glu Val Thr Trp Ala Lys Gln Gly Arg Thr Glu Arg
 Leu Cys Ser Gln Asn Pro Pro Val Leu Lys Arg His Gln Arg Glu Ile Thr Arg
 Thr Thr Leu Gln Ser Asp Gln Glu Glu Ile Asp Tyr Asp Thr Ile Ser Val Glu
 Met Lys Lys Glu Asp Phe Asp Ile Tyr Asp Glu Asp Glu Asn Gln Ser Pro Arg
 Ser Phe Gln Lys Lys Thr Arg His Tyr Phe Ile Ala Ala Val Glu Arg Leu Trp Asp
 Tyr Gly Met Ser Ser Ser Pro His Val Leu Arg Asn Arg Ala Gln Ser Gly Ser Val
 Pro Gln Phe Lys Lys Val Val Phe Gln Glu Phe Thr Asp Gly Ser Phe Thr Gln Pro
 Leu Tyr Arg Gly Glu Leu Asn Glu His Leu Gly Leu Leu Gly Pro Tyr Ile Arg
 Ala Glu Val Glu Asp Asn Ile Met Val Thr Phe Arg Asn Gln Ala Ser Arg Pro
 Tyr Ser Phe Tyr Ser Ser Leu Ile Ser Tyr Glu Glu Asp Gln Arg Gln Gly Ala Glu
 Pro Arg Lys Asn Phe Val Lys Pro Asn Glu Thr Lys Thr Tyr Phe Trp Lys Val
 Gln His His Met Ala Pro Thr Lys Asp Glu Phe Asp Cys Lys Ala Trp Ala Tyr
 Phe Ser Asp Val Asp Leu Glu Lys Asp Val His Ser Gly Leu Ile Gly Pro Leu
 Leu Val Cys His Thr Asn Thr Leu Asn Pro Ala His Gly Arg Gln Val Thr Val Gln
 Glu Phe Ala Leu Phe Phe Thr Ile Phe Asp Glu Thr Lys Ser Trp Tyr Phe Thr Glu
 Asn Met Glu Arg Asn Cys Arg Ala Pro Cys Asn Ile Gln Met Glu Asp Pro Thr
 Phe Lys Glu Asn Tyr Arg Phe His Ala Ile Asn Gly Tyr Ile Met Asp Thr Leu Pro
 Gly Leu Val Met Ala Gln Asp Gln Arg Ile Arg Trp Tyr Leu Leu Ser Met Gly
 Ser Asn Glu Asn Ile His Ser Ile His Phe Ser Gly His Val Phe Thr Val Arg Lys
 Lys Glu Glu Tyr Lys Met Ala Leu Tyr Asn Leu Tyr Pro Gly Val Phe Glu Thr
 Val Glu Met Leu Pro Ser Lys Ala Gly Ile Trp Arg Val Glu Cys Leu Ile Gly Glu
 His Leu His Ala Gly Met Ser Thr Leu Phe Leu Val Tyr Ser Asn Lys Cys Gln Thr
 Pro Leu Gly Met Ala Ser Gly His Ile Arg Asp Phe Gln Ile Thr Ala Ser Gly Gln
 Tyr Gly Gln Trp Ala Pro Lys Leu Ala Arg Leu His Tyr Ser Gly Ser Ile Asn Ala
 Trp Ser Thr Lys Glu Pro Phe Ser Trp Ile Lys Val Asp Leu Leu Ala Pro Met Ile
 Ile His Gly Ile Lys Thr Gln Gly Ala Arg Gln Lys Phe Ser Ser Leu Tyr Ile Ser
 Gln Phe Ile Ile Met Tyr Ser Leu Asp Gly Lys Lys Trp Gln Thr Tyr Arg Gly
 Asn Ser Thr Gly Thr Leu Met Val Phe Phe Gly Asn Val Asp Ser Ser Gly Ile
 Lys His Asn Ile Phe Asn Pro Pro Ile Ile Ala Arg Tyr Ile Arg Leu His Pro Thr
 His Tyr Ser Ile Arg Ser Thr Leu Arg Met Glu Leu Met Gly Cys Asp Leu Asn
 Ser Cys Ser Met Pro Leu Gly Met Glu Ser Lys Ala Ile Ser Asp Ala Gln Ile Thr
 Ala Ser Ser Tyr Phe Thr Asn Met Phe Ala Thr Trp Ser Pro Ser Lys Ala Arg Leu
 His Leu Gln Gly Arg Ser Asn Ala Trp Arg Pro Gln Val Asn Asn Pro Lys Glu
 Trp Leu Gln Val Asp Phe Gln Lys Thr Met Lys Val Thr Gly Val Thr Thr Gln
 Gly Val Lys Ser Leu Leu Thr Ser Met Tyr Val Lys Glu Phe Leu Ile Ser Ser Ser
 Gln Asp Gly His Gln Trp Thr Leu Phe Phe Gln Asn Gly Lys Val Lys Val Phe
 Gln Gly Asn Gln Asp Ser Phe Thr Pro Val Val Asn Ser Leu Asp Pro Pro Leu
 Leu Thr Arg Tyr Leu Arg Ile His

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FIG.65B-4

Pro Gln Ser Trp Val His Gln Ile Ala Leu Arg Met Glu Val Leu Gly Cys Glu
Ala Gln Asp Leu Tyr

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FIG. 66A

TCCACCTGTCCCCGCAGCGCCGGCTCGCGCCCTCCTGCCGCAGCCACC
GAGCCGCCGTCTAGCGCCCCGACCTCGCCACCATGAGAGCCCTGCTG
GCGCGCCTGCTTCTCTGCGTCCTGGTCTGTGAGCGACTCCAAAGGCAGC
AATGAACTTCATCAAGTTCATCGAACTGTGACTGTCTAAATGGAGGA
ACATGTGTGTCCAACAAGTACTTCTCCAACATTCACTGGTGCAACTGC
CCAAAGAAAATTCGGAGGGCAGCACTGTGAAATAGATAAGTCAAAAAC
CTGCTATGAGGGGAATGGTCACTTTACCGAGGAAAGGCCAGCACTG
ACACCATGGGCCGGCCCTGCCCTGGAACCTGCCACTGTCCTTC
AGCAAACGTACCATGCCACAGATCTGATGCTCTTCAGCTGGGCTGG
GGAAACATAATTACTGCAAGAACCCAGACAACCGGAGGCGACCCCTGG
TGCTATGTGCAGGTGGGCCCTAAAGCCGCTTGTCGAAGAGTGCATGGT
GCATGACTGCGCAGATGGAAAAAGCCCTCCTCTCCTCCAGAAGAAT
TAAATTTTCAGTGTGGCCAAAAGACTCTGAGGCCCGCTTTAAGATTA
TTGGGGGAGAATTCACCACCATCGAGAACCAGCCCTGGTTTTCGGCC
ATCTACAGGAGGCACCGGGGGGGCTCTGTACCTACGTGTGTGGAGG
CAGCCTCATCAGCCCTTGCTGGGTGATCAGCGCCACACACTGCTTCAT
TGATTACCCAAAGAAGGAGGACTACATCGTCTACCTGGGTGCTCAA
GGCTTAACTCCAACACGCAAGGGGAGATGAAGTTTGAGGTGGAAAAAC
CTCATCTACACAAGGACTACAGCGCTGACACGCTTGCTCACCACAAC
GACATTGCCTTGCTGAAGATCCGTTCCAAGGAGGGCAGGTGTGCGCA
GCCATCCCGGACTATACAGACCATCTGCCTGCCCTCGATGTATAACGA
TCCCCAGTTTGGCACAAGCTGTGAGATCACTGGCTTTGGAAAAGAGA
ATTCTACCGACTATCTCTATCCGGAGCAGCTGAAGATGACTGTTGTGA
AGCTGATTTCACCGGGAGTGTGACGAGCCCCACTACTACGGCTCTG
AAGTCACCACCAAAATGCTGTGTGCTGCTGACCCACAGTGGA AAAACA
GATTCCTGCCAGGGAGACTCAGGGGGACCCCTCGTCTGTTCCCTCCAA
GGCCGCATGACTTTGACTGGAATTGTGAGCTGGGGCCGTGGATGTGC
CCTGAAGGACAAGCCAGGCGTCTACACGAGAGTCTCACACTTCTTAC
CCTGGATCCGCAGTCACACCAAGGAAGAGAATGGCCTGGCCCTCTGA
GGGTCCCCAGGGAGGAAACGGGCACCCCGCTTCTGTCTGGTTGTG
ATTTTTCAGTAGAGTCATCTCCATCAGCTGTAAGAAGAGACTGGGA
AGAT

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FIG. 66B

Met Arg Ala Leu Leu Ala Arg Leu Leu Leu Cys Val Leu Val Val Ser Asp Ser
Lys Gly Ser Asn Glu Leu His Gln Val Pro Ser Asn Cys Asp Cys Leu Asn Gly
Gly Thr Cys Val Ser Asn Lys Tyr Phe Ser Asn Ile His Trp Cys Asn Cys Pro Lys
Lys Phe Gly Gly Gln His Cys Glu Ile Asp Lys Ser Lys Thr Cys Tyr Glu Gly Asn
Gly His Phe Tyr Arg Gly Lys Ala Ser Thr Asp Thr Met Gly Arg Pro Cys Leu Pro
Trp Asn Ser Ala Thr Val Leu Gln Gln Thr Tyr His Ala His Arg Ser Asp Ala Leu
Gln Leu Gly Leu Gly Lys His Asn Tyr Cys Arg Asn Pro Asp Asn Arg Arg Arg
Pro Trp Cys Tyr Val Gln Val Gly Leu Lys Pro Leu Val Gln Glu Cys Met Val His
Asp Cys Ala Asp Gly Lys Lys Pro Ser Ser Pro Pro Glu Glu Leu Lys Phe Gln Cys
Gly Gln Lys Thr Leu Arg Pro Arg Phe Lys Ile Ile Gly Gly Glu Phe Thr Thr Ile
Glu Asn Gln Pro Trp Phe Ala Ala Ile Tyr Arg Arg His Arg Gly Gly Ser Val Thr
Tyr Val Cys Gly Gly Ser Leu Ile Ser Pro Cys Trp Val Ile Ser Ala Thr His Cys
Phe Ile Asp Tyr Pro Lys Lys Glu Asp Tyr Ile Val Tyr Leu Gly Arg Ser Arg Leu
Asn Ser Asn Thr Gln Gly Glu Met Lys Phe Glu Val Glu Asn Leu Ile Leu His Lys
Asp Tyr Ser Ala Asp Thr Leu Ala His His Asn Asp Ile Ala Leu Leu Lys Ile Arg
Ser Lys Glu Gly Arg Cys Ala Gln Pro Ser Arg Thr Ile Gln Thr Ile Cys Leu Pro
Ser Met Tyr Asn Asp Pro Gln Phe Gly Thr Ser Cys Glu Ile Thr Gly Phe Gly Lys
Glu Asn Ser Thr Asp Tyr Leu Tyr Pro Glu Gln Leu Lys Met Thr Val Val Lys
Leu Ile Ser His Arg Glu Cys Gln Gln Pro His Tyr Tyr Gly Ser Glu Val Thr Thr
Lys Met Leu Cys Ala Ala Asp Pro Gln Trp Lys Thr Asp Ser Cys Gln Gly Asp
Ser Gly Gly Pro Leu Val Cys Ser Leu Gln Gly Arg Met Thr Leu Thr Gly Ile Val
Ser Trp Gly Arg Gly Cys Ala Leu Lys Asp Lys Pro Gly Val Tyr Thr Arg Val Ser
His Phe Leu Pro Trp Ile Arg Ser His Thr Lys Glu Glu Asn Gly Leu Ala Leu

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FIG. 67A

TCCTGCACAGGCAGTGCCTTGAAGTGCTTCTTCAGAGACCTTTCTTCA
TAGACTACTTTTTTTTCTTTAAGCAGCAAAAGGAGAAAAATTGTCATCA
AGGATATTCCAGATTCTTGACAGCATTCTCGTCATCTCTGAGGACATC
ACCATCATCTCAGGATGAGGGGCATGAAGCTGCTGGGGGCGCTGCTG
GCACTGGCGGCCCTACTGCAGGGGGCCGTGTCCCTGAAGATCGCAGC
CTTCAACATCCAGACATTTGGGGAGACCAAGATGTCCAATGCCACCCT
CGTCAGCTACATTGTGCAGATCCTGAGCCGCTATGACATCGCCCTGGT
CCAGGAGGTCAGAGACAGCCACCTGACTGCCGTGGGGAAGCTGCTGG
ACAACCTCAATCAGGATGCACCAGACACCTATCACTACGTGGTCAGT
GAGCCACTGGGACGGAACAGCTATAAGGAGCGCTACCTGTTCTGTGTA
CAGGCCCTGACCAGGTGTCTGCGGTGGACAGCTACTACTACGATGATG
GCTGCGAGCCCTGCGGGAACGACACCTTCAACCGAGAGCCAGCCATT
GTCAGGTTCTTCTCCCGTTTACAGAGGTCAGGGAGTTTGCCATTGTT
CCCCTGCATGCGGCCCCGGGGGACGCAGTAGCCGAGATCGACGCTCT
CTATGACGTCTACCTGGATGTCCAAGAGAAAATGGGGCTTGGAGGACG
TCATGTTGATGGGCGACTTCAATGCGGGCTGCAGCTATGTGAGACCCT
CCCAGTGGTCATCCATCCGCCTGTGGACAAGCCCCACCTTCCAGTGCG
TGATCCCCGACAGCGCTGACACCACAGCTACACCCACGCACTGTGCCT
ATGACAGGATCGTGGTTGCAGGGATGCTGCTCCGAGGGCGCCGTTGTT
CCGACTCGGCTCTTCCCTTTAACTTCCAGGCTGCCTATGGCCTGAGTG
ACCAACTGGCCCAAGCCATCAGTGACCACTATCCAGTGGAGGTGATG
CTGAAGTGAGCAGCCCCTCCCCACACCAGTTGAAGTGCAG

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FIG. 67B

Met Arg Gly Met Lys Leu Leu Gly Ala Leu Leu Ala Leu Ala Leu Leu Gln
Gly Ala Val Ser Leu Lys Ile Ala Ala Phe Asn Ile Gln Thr Phe Gly Glu Thr Lys
Met Ser Asn Ala Thr Leu Val Ser Tyr Ile Val Gln Ile Leu Ser Arg Tyr Asp Ile
Ala Leu Val Gln Glu Val Arg Asp Ser His Leu Thr Ala Val Gly Lys Leu Leu
Asp Asn Leu Asn Gln Asp Ala Pro Asp Thr Tyr His Tyr Val Val Ser Glu Pro
Leu Gly Arg Asn Ser Tyr Lys Glu Arg Tyr Leu Phe Val Tyr Arg Pro Asp Gln
Val Ser Ala Val Asp Ser Tyr Tyr Tyr Asp Asp Gly Cys Glu Pro Cys Gly Asn
Asp Thr Phe Asn Arg Glu Pro Ala Ile Val Arg Phe Phe Ser Arg Phe Thr Glu Val
Arg Glu Phe Ala Ile Val Pro Leu His Ala Ala Pro Gly Asp Ala Val Ala Glu Ile
Asp Ala Leu Tyr Asp Val Tyr Leu Asp Val Gln Glu Lys Trp Gly Leu Glu Asp
Val Met Leu Met Gly Asp Phe Asn Ala Gly Cys Ser Tyr Val Arg Pro Ser Gln
Trp Ser Ser Ile Arg Leu Trp Thr Ser Pro Thr Phe Gln Trp Leu Ile Pro Asp Ser
Ala Asp Thr Thr Ala Thr Pro Thr His Cys Ala Tyr Asp Arg Ile Val Val Ala Gly
Met Leu Leu Arg Gly Ala Val Val Pro Asp Ser Ala Leu Pro Phe Asn Phe Gln
Ala Ala Tyr Gly Leu Ser Asp Gln Leu Ala Gln Ala Ile Ser Asp His Tyr Pro Val
Glu Val Met Leu Lys

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FIG. 68A

GCTGCATCAGAAGAGGGCCATCAAGCACATCACTGTCCTTCTGCCATGG
CCCTGTGGATGCGCCTCCTGCCCCCTGCTGGCGCTGCTGGCCCTCTGGG
GACCTGACCCAGCCGAGCCCTTGTGAACCAACACCTGTGCGGCTCAC
ACCTGGTGGAAGCTCTCTACCTAGTGTGCGGGGAACGAGGCTTCTTCT
ACACACCCAAGACCCGCCGGGAGGCAGAGGACCTGCAGGTGGGGCA
GGTGGAGCTGGGCGGGGGCCCTGGTGCAGGCAGCCTGCAGCCCTTGG
CCCTGGAGGGGTCCCTGCAGAAGCGTGGCATTGTGGAACAATGCTGT
ACCAGCATCTGCTCCCTCTACCAGCTGGAGAACTACTGCAACTAGACG
CAGCCCGCAGGCAGCCCCCACC CGCCCTCCTGCACCGAGAGAGA
TGAATAAAGCCCTTGAACCAGC

FIG. 68B

Met Ala Leu Trp Met Arg Leu Leu Pro Leu Leu Ala Leu Leu Ala Leu Trp Gly
Pro Asp Pro Ala Ala Ala Phe Val Asn Gln His Leu Cys Gly Ser His Leu Val
Glu Ala Leu Tyr Leu Val Cys Gly Glu Arg Gly Phe Phe Tyr Thr Pro Lys Thr
Arg Arg Glu Ala Glu Asp Leu Gln Val Gly Gln Val Glu Leu Gly Gly Gly Pro
Gly Ala Gly Ser Leu Gln Pro Leu Ala Leu Glu Gly Ser Leu Gln Lys Arg Gly Ile
Val Glu Gln Cys Cys Thr Ser Ile Cys Ser Leu Tyr Gln Leu Glu Asn Tyr Cys Asn

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FIG. 69A

ATGGGAGGTTGGTCTTCCAAACCTCGACAAGGCATGGGGACGAATCT
TTCTGTTCCCAATCCTCTGGGATTCTTTCCCGATCACCAGTTGGACCCCT
GCGTTCGGAGCCAACTCAAACAATCCAGATTGGGACTTCAACCCCAA
CAAGGATCACTGGCCAGAGGCAATCAAGGTAGGAGCGGGAGACTTC
GGGCCAGGGTTACCCCCACCACACGGCGGTCTTTTGGGGTGGAGCCC
TCAGGCTCAGGGCATATTGACAACAGTGCCAGCAGCGCCTCCTCCTG
TTTCCACCAATCGGCAGTCAGGAAGACAGCCTACTCCCATCTCTCCAC
CTCTAAGAGACAGTCATCCTCAGGCCATGCAGTGGAACCTCCACAACA
TTCCACCAAGCTCTGCTAGATCCCAGAGTGAGGGGCTATATTTTCCT
GCTGGTGGCTCCAGTTCGGGAACAGTAAACCTGTTCGGACTACTGTC
TCACCCATATCGTCAATCTTCTCGAGGACTGGGGACCCCTGCACCGAAC
ATGGAGAGCACAACATCAGGATTCTAGGACCCCTGCTCGTGTACA
GGCGGGGTTTTTCTTGTTGACAAGAATCCTCAATACACAGAGTCT
AGACTCGTGGTGGACTTCTCTCAATTTCTAGGGGGAGCACCCACGTG
TCCTGGCCAAAATTTCGAGTCCCCAACCTCCAATCACTCACCAACCTC
TTGTCTCCAATTTGTCTGGTTATCGCTGGATGTGTCTGCGGCGTTTT
ATCATATTCTCTTCATCCTGCTGCTATGCCTCATCTTCTTGTTGGTTC
TTCTGGACTACCAAGGTATGTTGCCCGTTTGTCTCTACTTCCAGGAA
CATCAACTACCAGCACGGGACCATGCAAGACCTGCACGATTCTGCT
CAAGGAACCTCTATGTTTCCCTCTTGTTGCTGTACAAAACCTTCGGAC
GGAAACTGCACTTGTAATCCCATCCCATCATCCTGGGCTTTCGCAAGA
TTCTATGGGAGTGGGCTCAGTCCGTTTCTCCTGGCTCAGTTTACTA
GTGCCATTTGTTTCACTGGTTTCGAGGGCTTTCCCCACTGTTTGGCTTT
CAGTTATATGGATGATGTGGTATTGGGGGCCAAGTCTGTACAACATCT
TGAGTCCCTTTTTACCTCTATTACCAATTTTCTTTTGTCTTTGGGTATAC
ATTGA

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FIG. 69B

Met Gly Gly Trp Ser Ser Lys Pro Arg Gln Gly Met Gly Thr Asn Leu Ser Val Pro
Asn Pro Leu Gly Phe Phe Pro Asp His Gln Leu Asp Pro Ala Phe Gly Ala Asn
Ser Asn Asn Pro Asp Trp Asp Phe Asn Pro Asn Lys Asp His Trp Pro Glu Ala Ile
Lys Val Gly Ala Gly Asp Phe Gly Pro Gly Phe Thr Pro Pro His Gly Gly Leu Leu
Gly Trp Ser Pro Gln Ala Gln Gly Ile Leu Thr Thr Val Pro Ala Ala Pro Pro Pro
Val Ser Thr Asn Arg Gln Ser Gly Arg Gln Pro Thr Pro Ile Ser Pro Pro Leu Arg
Asp Ser His Pro Gln Ala Met Gln Trp Asn Ser Thr Thr Phe His Gln Ala Leu Leu
Asp Pro Arg Val Arg Gly Leu Tyr Phe Pro Ala Gly Gly Ser Ser Ser Gly Thr Val
Asn Pro Val Pro Thr Thr Val Ser Pro Ile Ser Ser Ile Phe Ser Arg Thr Gly Asp
Pro Ala Pro Asn Met Glu Ser Thr Thr Ser Gly Phe Leu Gly Pro Leu Leu Val Leu
Gln Ala Gly Phe Phe Leu Leu Thr Arg Ile Leu Thr Ile Pro Gln Ser Leu Asp Ser
Trp Trp Thr Ser Leu Asn Phe Leu Gly Gly Ala Pro Thr Cys Pro Gly Gln Asn Ser
Gln Ser Pro Thr Ser Asn His Ser Pro Thr Ser Cys Pro Pro Ile Cys Pro Gly Tyr
Arg Trp Met Cys Leu Arg Arg Phe Ile Ile Phe Leu Phe Ile Leu Leu Leu Cys Leu
Ile Phe Leu Leu Val Leu Leu Asp Tyr Gln Gly Met Leu Pro Val Cys Pro Leu
Leu Pro Gly Thr Ser Thr Thr Ser Thr Gly Pro Cys Lys Thr Cys Thr Ile Pro Ala
Gln Gly Thr Ser Met Phe Pro Ser Cys Cys Cys Thr Lys Pro Ser Asp Gly Asn
Cys Thr Cys Ile Pro Ile Pro Ser Ser Trp Ala Phe Ala Arg Phe Leu Trp Glu Trp
Ala Ser Val Arg Phe Ser Trp Leu Ser Leu Leu Val Pro Phe Val Gln Trp Phe Ala
Gly Leu Ser Pro Thr Val Trp Leu Ser Val Ile Trp Met Met Trp Tyr Trp Gly Pro
Ser Leu Tyr Asn Ile Leu Ser Pro Phe Leu Pro Leu Leu Pro Ile Phe Phe Cys Leu
Trp Val Tyr Ile

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FIG. 70A

CGAACCACCTCAGGGTCCTGTGGACAGCTCACCTAGCTGCAATGGCTA
CAGGCTCCCGGACGTCCCTGCTCCTGGCTTTTGGCCTGCTCTGCCTGC
CCTGGCTTCAAGAGGGCAGTGCCTTCCCAACCATTCCTTATCCAGGC
CTTTTGACAACGCTATGCTCCGCGCCCATCGTCTGCACCAGCTGGCCT
TTGACACCTACCAGGAGTTTGAAGAAGCCTATATCCCAAAGGAACAG
AAGTATTTCATTCTGCAGAACCCCCAGACCTCCCTCTGTTTCTCAGAG
TCTATTCCGACACCCTCCAACAGGGAGGAAACACAACAGAAATCCAA
CCTAGAGCTGCTCCGCATCTCCCTGCTGCTCATCCAGTCGTGGCTGGA
GCCCCGTGCAGTTCCTCAGGAGTGTCTTCGCCAACAGCCTGGTGTACGG
CGCCTCTGACAGCAACGCTCTATGACCTCCTAAAGGACCTAGAGGAAG
GCATCCAAAACGCTGATGGGGAGGCTGGAAGATGGCAGCCCCCGGACT
GGGCAGATCTTCAAGCAGACCTACAGCAAGTTCGACACAAACTCACA
CAACGATGACGCACTACTCAAGAACTACGGGCTGCTCTACTGCTTCAG
GAAGGACATGGCAAGGTCGAGACATTCCTGCGCATCGTGCAGTGCCG
CTCTGTGGAGGGCAGCTGTGGCTTCTAGCTGCCCGGGTGGCATCCCTG
TGACCCCTCCCCAGTGCCTCTCCTGGCCCTGGAAGTTGCCACTCCAGT
GCCACCAGCCTTGCTTAATAAAATTAAGTTGCATC

FIG. 70B

Met Ala Thr Gly Ser Arg Thr Ser Leu Leu Leu Ala Phe Gly Leu Leu Cys Leu
Pro Trp Leu Gln Glu Gly Ser Ala Phe Pro Thr Ile Pro Leu Ser Arg Pro Phe Asp
Asn Ala Met Leu Arg Ala His Arg Leu His Gln Leu Ala Phe Asp Thr Tyr Gln
Glu Phe Glu Glu Ala Tyr Ile Pro Lys Glu Gln Lys Tyr Ser Phe Leu Gln Asn Pro
Gln Thr Ser Leu Cys Phe Ser Glu Ser Ile Pro Thr Pro Ser Asn Arg Glu Glu Thr
Gln Gln Lys Ser Asn Leu Glu Leu Leu Arg Ile Ser Leu Leu Leu Ile Gln Ser Trp
Leu Glu Pro Val Gln Phe Leu Arg Ser Val Phe Ala Asn Ser Leu Val Tyr Gly Ala
Ser Asp Ser Asn Val Tyr Asp Leu Leu Lys Asp Leu Glu Glu Gly Ile Gln Thr Leu
Met Gly Arg Leu Glu Asp Gly Ser Pro Arg Thr Gly Gln Ile Phe Lys Gln Thr Tyr
Ser Lys Phe Asp Thr Asn Ser His Asn Asp Asp Ala Leu Leu Lys Asn Tyr Gly
Leu Leu Tyr Cys Phe Arg Lys Asp Met Asp Lys Val Glu Thr Phe Leu Arg Ile
Val Gln Cys Arg Ser Val Glu Gly Ser Cys Gly Phe

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FIG. 71A

ATGGCGCCCGTCGCCGTCTGGGCGCGCTGGCCGTCGGACTGGAGCT
CTGGGCTGCGGCGCACGCCTTGCCCCGCCAGGTGGCATTTACACCCTA
CGCCCCGGAGCCCCGGGAGCACATGCCGGCTCAGAGAATACTATGACC
AGACAGCTCAGATGTGCTGCAGCAAATGCTCGCCGGGCCAACATGCA
AAAGTCTTCTGTACCAAGACCTCGGACACCGTGTGTGACTCCTGTGAG
GACAGCACATACACCAGCTCTGGAAGTGGGTTCGCCAGTGTGAG
CTGTGGCTCCCGCTGTAGCTCTGACCAGGTGGAAACTCAAGCCTGCAC
TCGGGAACAGAACCGCATCTGCACCTGCAGGCCCGGCTGGTACTGCG
CGCTGAGCAAGCAGGAGGGGTGCCGGCTGTGCGCGCCGTGCGCAAG
TGCCGCCCGGGCTTCGGCGTGGCCAGACCAGGAAGTGAACATCAGA
CGTGGTGTGCAAGCCCTGTGCCCCGGGGACGTTCTCCAACACGACTTC
ATCCACGGATATTTGCAGGCCCCACAGATCTGTAACTGGTGGCCAT
CCCTGGGAATGCAAGCATGGATGCAGTCTGCACGTCCACGTCCCCCA
CCCGGAGTATGGCCCCAGGGGCAGTACACTTACCCAGCCAGTGTCC
ACACGATCCCAACACACGCAGCCAACTCCAGAACCCAGCACTGTCC
AAGCACCTCCTTCTGCTCCCAATGGGCCCCAGCCCCCAGCTGAAGG
GAGCACTGGCGACTTCGCTCTTCCAGTTGGACTGATTGTGGGTGTGAC
AGCCTTGGGTCTACTAATAATAGGAGTGGTGAAGTGTGTATCATGAC
CCAGGTGAAAAAGAAGCCCTTGTGCCTGCAGAGAGAAGCCAAGGTGC
CTCACTTGCCTGCCGATAAGGCCCGGGGTACACAGGGCCCCGAGCAG
CAGCACCTGCTGATCACAGCGCCGAGCTCCAGCAGCAGCTCCCTGGA
GAGCTCGGCCAGTGCGTTGGACAGAAGGGCGCCCACTCGGAACCAGC
CACAGGCACCAGGCGTGGAGGCCAGTGGGGCCGGGGAGGCCCGGGC
CAGCACCGGGAGCTCAGATTCTTCCCCTGGTGGCCATGGGACCCAGG
TCAATGTCACTGCATCGTGAACGTCTGTAGCAGCTCTGACCACAGCT
CACAGTGCTCTCTCCCAAGCCAGCTCCACAATGGGAGACACAGATTCC
AGCCCCCTCGGAGTCCCCGAAGGACGAGCAGTCCCCCTTCTCCAAGGA
GGAATGTGCCTTTTCGCTCACAGCTGGAGACGCCAGAGACCCTGTGG
GGAGCACCGAAGAGAAGCCCCCTGCCCCCTTGGAGTGCCTGATGCTGG
ATGAAGCCCAGTTAACCAGGCCGGTGTGGGCTGTGTCTGAGCCAAGG
TGGGCTGAGCCCTGGCAGGATGACCCTGCGAAGGGGGCCCTGGTCTT
CCAGG

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FIG. 71B

Met Ala Pro Val Ala Val Trp Ala Ala Leu Ala Val Gly Leu Glu Leu Trp Ala Ala
Ala His Ala Leu Pro Ala Gln Val Ala Phe Thr Pro Tyr Ala Pro Glu Pro Gly Ser
Thr Cys Arg Leu Arg Glu Tyr Tyr Asp Gln Thr Ala Gln Met Cys Cys Ser Lys
Cys Ser Pro Gly Gln His Ala Lys Val Phe Cys Thr Lys Thr Ser Asp Thr Val Cys
Asp Ser Cys Glu Asp Ser Thr Tyr Thr Gln Leu Trp Asn Trp Val Pro Glu Cys
Leu Ser Cys Gly Ser Arg Cys Ser Ser Asp Gln Val Glu Thr Gln Ala Cys Thr Arg
Glu Gln Asn Arg Ile Cys Thr Cys Arg Pro Gly Trp Tyr Cys Ala Leu Ser Lys Gln
Glu Gly Cys Arg Leu Cys Ala Pro Leu Arg Lys Cys Arg Pro Gly Phe Gly Val
Ala Arg Pro Gly Thr Glu Thr Ser Asp Val Val Cys Lys Pro Cys Ala Pro Gly Thr
Phe Ser Asn Thr Thr Ser Ser Thr Asp Ile Cys Arg Pro His Gln Ile Cys Asn Val
Val Ala Ile Pro Gly Asn Ala Ser Met Asp Ala Val Cys Thr Ser Thr Ser Pro Thr
Arg Ser Met Ala Pro Gly Ala Val His Leu Pro Gln Pro Val Ser Thr Arg Ser Gln
His Thr Gln Pro Thr Pro Glu Pro Ser Thr Ala Pro Ser Thr Ser Phe Leu Leu Pro
Met Gly Pro Ser Pro Pro Ala Glu Gly Ser Thr Gly Asp Phe Ala Leu Pro Val Gly
Leu Ile Val Gly Val Thr Ala Leu Gly Leu Leu Ile Ile Gly Val Val Asn Cys Val
Ile Met Thr Gln Val Lys Lys Lys Pro Leu Cys Leu Gln Arg Glu Ala Lys Val Pro
His Leu Pro Ala Asp Lys Ala Arg Gly Thr Gln Gly Pro Glu Gln Gln His Leu Leu
Ile Thr Ala Pro Ser Ser Ser Ser Ser Ser Leu Glu Ser Ser Ala Ser Ala Leu Asp Arg
Arg Ala Pro Thr Arg Asn Gln Pro Gln Ala Pro Gly Val Glu Ala Ser Gly Ala Gly
Glu Ala Arg Ala Ser Thr Gly Ser Ser Ser Asp Ser Pro Gly Gly His Gly Thr Gln
Val Asn Val Thr Cys Ile Val Asn Val Cys Ser Ser Ser Ser Asp His Ser Ser Gln Cys
Ser Ser Gln Ala Ser Ser Thr Met Gly Asp Thr Asp Ser Ser Pro Ser Glu Ser Pro
Lys Asp Glu Gln Val Pro Phe Ser Lys Glu Glu Cys Ala Phe Arg Ser Gln Leu Glu
Thr Pro Glu Thr Leu Leu Gly Ser Thr Glu Glu Lys Pro Leu Pro Leu Gly Val Pro
Asp Ala Gly Met Lys Pro Ser

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FIG. 72A

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val
Thr Ile Thr Cys Arg Ala Ser Gln Asp Val Asn Thr Ala Val Ala Trp Tyr Gln Gln
Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Ser Ala Ser Phe Leu Tyr Ser Gly
Val Pro Ser Arg Phe Ser Gly Ser Arg Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser
Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln His Tyr Thr Thr Pro
Pro Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys

FIG. 72B

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Arg
Leu Ser Cys Ala Ala Ser Gly Phe Asn Ile Lys Asp Thr Tyr Ile His Trp Val Arg
Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Tyr Pro Thr Asn Gly Tyr
Thr Arg Tyr Ala Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Ala Asp Thr Ser Lys
Asn Thr Ala Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr
Tyr Cys Ser Arg Trp Gly Gly Asp Gly Phe Tyr Ala Met Asp Tyr Trp Gly Gln
Gly Thr Leu Val Thr Val Ser Ser

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FIG. 73A

Gln Val Thr Leu Arg Glu Ser Gly Pro Ala Leu Val Lys Pro Thr Gln Thr Leu Thr
Leu Thr Cys Thr Phe Ser Gly Phe Ser Leu Ser Thr Ser Gly Met Ser Val Gly Trp
Ile Arg Gln Pro Ser Gly Lys Ala Leu Glu Trp Leu Ala Asp Ile Trp Trp Asp Asp
Lys Lys Asp Tyr Asn Pro Ser Leu Lys Ser Arg Leu Thr Ile Ser Lys Asp Thr Ser
Lys Asn Gln Val Val Leu Lys Val Thr Asn Met Asp Pro Ala Asp Thr Ala Thr
Tyr Tyr Cys Ala Arg Ser Met Ile Thr Asn Trp Tyr Phe Asp Val Trp Gly Ala Gly
Thr Thr Val Thr Val Ser Ser

FIG. 73B

Asp Ile Gln Met Thr Gln Ser Pro Ser Thr Leu Ser Ala Ser Val Gly Asp Arg Val
Thr Ile Thr Cys Lys Cys Gln Leu Ser Val Gly Tyr Met His Trp Tyr Gln Gln Lys
Pro Gly Lys Ala Pro Lys Leu Trp Ile Tyr Asp Thr Ser Lys Leu Ala Ser Gly Val
Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser
Leu Gln Pro Asp Asp Phe Ala Thr Tyr Tyr Cys Phe Gln Gly Ser Gly Tyr Pro Phe
Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys

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FIG. 74A

GACATCTTGCTGACTCAGTCTCCAGCCATCCTGTCTGTGAGTCCAGGA
 GAAAGAGTCAGTTTCTCCTGCAGGGCCAGTCAGTTCGTTGGCTCAAGC
 ATCCACTGGTATCAGCAAAAGAACAATGGTTCTCCAAGGCTTCTCATA
 AAGTATGCTTCTGAGTCTATGTCTGGGATCCCTTCCAGGTTTAGTGGC
 AGTGGATCAGGGACAGATTTTACTCTTAGCATCAACACTGTGGAGTCT
 GAAGATATTGCAGATTATTACTGTCAACAAAGTCATAGCTGGCCATTC
 ACGTTCGGCTCGGGGACAAATTTGGAAGTAAAAGAAGTGAAGCTTGA
 GGAGTCTGGAGGAGGCTTGGTGCAACCTGGAGGATCCATGAAACTCT
 CCTGTGTTGCCTCTGGATTCAATTTTCAGTAACCACTGGATGAACTGGG
 TCCGCCAGTCTCCAGAGAAGGGGCTTGAGTGGGTTGCTGAAATTAGA
 TCAAAATCTATTAATTCTGCAACACATTATGCGGAGTCTGTGAAAGGG
 AGGTTCAACATCTCAAGAGATGATTCCAAAAGTGCTGTCTACCTGCAA
 ATGACCGACTTAAGAAGCTGAAGACACTGGCGTTTATTACTGTTCCAGG
 AATTACTACGGTAGTACCTACGACTACTGGGGCCAAGGCACCACTCTC
 ACAGTCTCC

FIG. 74B

Asp Ile Leu Leu Thr Gln Ser Pro Ala Ile Leu Ser Val Ser Pro Gly Glu Arg Val
 Ser Phe Ser Cys Arg Ala Ser Gln Phe Val Gly Ser Ser Ile His Trp Tyr Gln Gln
 Arg Thr Asn Gly Ser Pro Arg Leu Leu Ile Lys Tyr Ala Ser Glu Ser Met Ser Gly
 Ile Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Ser Ile Asn
 Thr Val Glu Ser Glu Asp Ile Ala Asp Tyr Tyr Cys Gln Gln Ser His Ser Trp Pro
 Phe Thr Phe Gly Ser Gly Thr Asn Leu Glu Val Lys Glu Val Lys Leu Glu Glu Ser
 Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Met Lys Leu Ser Cys Val Ala Ser Gly
 Phe Ile Phe Ser Asn His Trp Met Asn Trp Val Arg Gln Ser Pro Glu Lys Gly Leu
 Glu Trp Val Ala Glu Ile Arg Ser Lys Ser Ile Asn Ser Ala Thr His Tyr Ala Glu
 Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Ser Ala Val Tyr
 Leu Gln Met Thr Asp Leu Arg Thr Glu Asp Thr Gly Val Tyr Tyr Cys Ser Arg
 Asn Tyr Tyr Gly Ser Thr Tyr Asp Tyr Trp Gly Gln Gly Thr Thr Leu Thr Val Ser

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FIG. 75A

ATGGAGACAGACACACTCCTGTTATGGGTGCTGCTGCTCTGGGGTTCCA
GGTTCCACTGGTGACGTACGGCGAGGGCCCCGGAGCCTGCGGGGCAG
GGACGCGCCAGCCCCACGCCCTGCGTCCCGGCCGAGTGCTTCGACC
TGCTGGTCCGCCACTGCGTGGCCTGCGGGCTCCTGCGCACGCCGCGGC
CGAAACCGGCCGGGGCCAGCAGCCCTGCGCCCAGGACGGCGCTGCAG
CCGCAGGAGTCGGTGGGCGCGGGGGCCGGCGAGGCGGCGGTTCGACA
AAACTCACACATGCCCACCGTGCCACGACCTGAACTCCTGGGGGGA
CCGTCAGTCTTCCTCTTCCCCC AAAACCCAAGGACACCCTCATGATC
TCCCGGACCCCTGAGGTACATGCGTGGTGGTGACGTGAGCCACGA
AGACCCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGAGGTGC
ATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTA
CCGTGTGGTCAGCGTCCTACCGTCCTGCACCAGGACTGGCTGAATGG
CAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCA
TCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAG
GTGTACACCCTGCCCCCATCCCGGGATGAGCTGACCAAGAACCAGGT
CAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGT
GGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCAG
CCTCCCGTGTGGACTCCGACGGCTCCTTCTTCTCTACAGCAAGCTC
ACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTC
CGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGCCTCT
CCCTGTCTCCCGGGAAATGA

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FIG. 75B

Met Glu Thr Asp Thr Leu Leu Leu Trp Val Leu Leu Leu Trp Val Pro Gly Ser
Thr Gly Asp Val Arg Arg Gly Pro Arg Ser Leu Arg Gly Arg Asp Ala Pro Ala
Pro Thr Pro Cys Val Pro Ala Glu Cys Phe Asp Leu Leu Val Arg His Cys Val Ala
Cys Gly Leu Leu Arg Thr Pro Arg Pro Lys Pro Ala Gly Ala Ser Ser Pro Ala Pro
Arg Thr Ala Leu Gln Pro Gln Glu Ser Val Gly Ala Gly Ala Gly Glu Ala Ala Val
Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser
Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu
Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp
Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr
Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn
Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys
Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro
Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly
Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys
Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys

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FIG. 76

Asp Ile Gln Met Thr Gln Thr Thr Ser Ser Leu Ser Ala Ser Leu Gly Asp Arg Val
Thr Ile Ser Cys Arg Ala Ser Gln Asp Ile Asn Asn Tyr Leu Asn Trp Tyr Gln Gln
Lys Pro Asp Gly Ile Val Lys Leu Leu Ile Tyr Tyr Thr Ser Thr Leu His Ser Gly
Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr Ser Leu Thr Ile Ser
Asn Leu Glu Gln Glu Asp Ile Ala Thr Tyr Phe Cys Gln Gln Gly Asn Thr Leu Pro
Trp Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys

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FIG. 77

Gln Val Gln Leu Gln Gln Ser Gly Ala Glu Leu Val Gly Pro Gly Thr Ser Val Arg
Val Ser Cys Lys Ala Ser Gly Tyr Ala Phe Thr Asn Tyr Leu Ile Glu Trp Val Lys
Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile Gly Val Ile Tyr Pro Gly Ser Gly Gly
Thr Asn Tyr Asn Glu Lys Phe Lys Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Ser
Thr Thr Ala Tyr Met Gln Leu Ser Ser Leu Thr Ser Asp Asp Ser Ala Val Tyr Phe
Cys Ala Arg Arg Asp Gly Asn Tyr Gly Trp Phe Ala Tyr Trp Gly Arg Gly Thr
Leu Val Thr Val Ser Ala

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FIG. 78

Asp Ile Gln Met Thr Gln Thr Pro Ser Thr Leu Ser Ala Ser Val Gly Asp Arg Val
Thr Ile Ser Cys Arg Ala Ser Gln Asp Ile Asn Asn Tyr Leu Asn Trp Tyr Gln Gln
Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Tyr Thr Ser Thr Leu His Ser Gly
Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr Thr Leu Thr Ile Ser
Ser Leu Gln Pro Asp Asp Phe Ala Thr Tyr Phe Cys Gln Gln Gly Asn Thr Leu
Pro Trp Thr Phe Gly Gln Gly Thr Lys Val Glu Val Lys

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FIG. 79

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser Ser Val Lys
Val Ser Cys Lys Ala Ser Gly Tyr Ala Phe Thr Asn Tyr Leu Ile Glu Trp Val Arg
Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile Gly Val Ile Tyr Pro Gly Ser Gly Gly
Thr Asn Tyr Asn Glu Lys Phe Lys Gly Arg Val Thr Leu Thr Val Asp Glu Ser
Thr Asn Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr
Phe Cys Ala Arg Arg Asp Gly Asn Tyr Gly Trp Phe Ala Tyr Trp Gly Gln Gly
Thr Leu Val Thr Val Ser Ser

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FIG. 80

Asp Ile Gln Met Thr Gln Thr Pro Ser Thr Leu Ser Ala Ser Val Gly Asp Arg Val
Thr Ile Ser Cys Arg Ala Ser Gln Asp Ile Asn Asn Tyr Leu Asn Trp Tyr Gln Gln
Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Tyr Thr Ser Thr Leu His Ser Gly
Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr Thr Leu Thr Ile Ser
Ser Leu Gln Pro Asp Asp Phe Ala Thr Tyr Phe Cys Gln Gln Gly Asn Thr Leu
Pro Trp Thr Phe Gly Gln Gly Thr Lys Val Glu Val Lys Arg Thr Val Ala Ala Pro
Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val
Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val
Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys
Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys
His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys
Ser Phe Asn Arg Gly Glu Cys

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FIG. 81

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser Ser Val Lys
Val Ser Cys Lys Ala Ser Gly Tyr Ala Phe Thr Asn Tyr Leu Ile Glu Trp Val Arg
Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile Gly Val Ile Tyr Pro Gly Ser Gly Gly
Thr Asn Tyr Asn Glu Lys Phe Lys Gly Arg Val Thr Leu Thr Val Asp Glu Ser
Thr Asn Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr
Phe Cys Ala Arg Arg Asp Gly Asn Tyr Gly Trp Phe Ala Tyr Trp Gly Gln Gly
Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala
Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp
Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val
His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val
Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys
Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His
Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe
Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly
Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr
Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu
Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser
Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp
Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser
Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr
Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp
Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu
His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly

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FIG. 82A

ATGGATTTTCAGGTGCAGATTATCAGCTTCCTGCTAATCAGTGCTTCA
GTCATAATGTCCAGAGGGCAAATTGTTCTCTCCCAGTCTCCAGCAATC
CTGTCTGCATCTCCAGGGGAGAAGGTCACAATGACTTGCAGGGCCAG
CTCAAGTGTAAGTTACATCCACTGGTTCAGCAGAAGCCAGGATCCTC
CCCCAAACCCTGGATTTATGCCACATCCAACCTGGCTTCTGGAGTCCC
TGTTGCTTCAGTGGCAGTGGGTCTGGGACTTCTTACTCTCTACAAT
CAGCAGAGTGGAGGCTGAAGATGCTGCCACTTATTACTGCCAGCAGT
GGACTAGTAACCCACCCACGTTTCGGAGGGGGGACCAAGCTGGAATC
AAA

FIG. 82B

Met Asp Phe Gln Val Gln Ile Ile Ser Phe Leu Leu Ile Ser Ala Ser Val Ile Met Ser
Arg Gly Gln Ile Val Leu Ser Gln Ser Pro Ala Ile Leu Ser Ala Ser Pro Gly Glu
Lys Val Thr Met Thr Cys Arg Ala Ser Ser Val Ser Tyr Ile His Trp Phe Gln
Gln Lys Pro Gly Ser Ser Pro Lys Pro Trp Ile Tyr Ala Thr Ser Asn Leu Ala Ser
Gly Val Pro Val Arg Phe Ser Gly Ser Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile
Ser Arg Val Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Trp Thr Ser Asn
Pro Pro Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys

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FIG. 83A

ATGGGTTGGAGCCTCATCTTGCTCTTCCTTGTCGCTGTTGCTACGCGTG
TCCTGTCCCAGGTACAACCTGCAGCAGCCTGGGGCTGAGCTGGTGAAG
CCTGGGGCCTCAGTGAAGATGTCCTGCAAGGCTTCTGGCTACACATTT
ACCAGTTACAATATGCACTGGGTAACACAGACACCTGGTCGGGGCCCT
GGAATGGATTGGAGCTATTTATCCCGGAAATGGTGATACTTCCTACAA
TCAGAAGTTCAAAGGCAAGGCCACATTGACTGCAGACAAATCCTCCA
GCACAGCCTACATGCAGCTCAGCAGCCTGACATCTGAGGACTCTGCG
GTCTATTACTGTGCAAGATCGACTTACTACGGCGGTGACTGGTACTTC
AATGTCTGGGGCGCAGGGACCACGGTCACCGTCTCTGCA

FIG. 83B

Met Gly Trp Ser Leu Ile Leu Leu Phe Leu Val Ala Val Ala Thr Arg Val Leu Ser
Gln Val Gln Leu Gln Gln Pro Gly Ala Glu Leu Val Lys Pro Gly Ala Ser Val Lys
Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr Asn Met His Trp Val Lys
Gln Thr Pro Gly Arg Gly Leu Glu Trp Ile Gly Ala Ile Tyr Pro Gly Asn Gly Asp
Thr Ser Tyr Asn Gln Lys Phe Lys Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser
Ser Thr Ala Tyr Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr
Cys Ala Arg Ser Thr Tyr Tyr Gly Gly Asp Trp Tyr Phe Asn Val Trp Gly Ala Gly
Thr Thr Val Thr Val Ser Ala

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FIG. 84A

CAAAATCAACGGGACTTTCCAAAATGTCGTAACAACTCCGCCCATTTG
ACGCAAATGGGCGGTAGGCGTGTACGGTGGGAGGTCTATATAAGCAG
AGCTGGGTACGTCTCCACATTCAGTGATCAGCAGTAACACAGACCC
GTCGACATGGGTTGGAGCCTCATCTTGCTCTTCTTGTGCTGTTGCTA
CGCGTGTGCTAGCACCAAGGGCCCATCGGTCTTCCCCCTGGCACCT
CCTCCAAGAGCACCTCTGGGGGCACAGCGCCCTGGGCTGCCTGGTC
AAGGACTACTTCCCCGAACCGGTGACGGTGTCTGTGGAACCTCAGGCGC
CCTGACCAGCGGGGTGCACACCTTCCCGGTGTCTTACAGTCTCAGG
ACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTGGG
CACCCAGACCTACATCTGCAACGTGAATCACAAGCCCAGCAACACCA
AGGTGGACAAGAAAAGCAGAGCCCAAATCTTGTGACAAAACCTACACA
TGCCCAACCGTGGCCAGCACCTGAACTCCTGGGGGGACCGTCAGTCTTC
CTCTTCCCCCAAACCAAGGACACCTCATGATCTCCCGGACCCCT
GAGGTCAATGCGTGGTGGTGGACGTGAGCCACGAAGACCTGAGGT
CAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGA
CAAAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGC
GTCCTCACCGTCTGCACCAAGGACTGGCTGAATGGCAAGGACTACAA
GTGCAAGGTCTCAAACAAAGCCCTCCAGCCCCCATCGAGAAAACCA
TCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCTG
CCCCATCCCGGGATGAGCTGACCAGGAACCAGGTACGCTGACCTG
CCTGGTCAAAGGCTTCTATCCAGCGACATCGCCGTGGAGTGGGAGA
GCAATGGGCAGCCGGAGAACAACCTACAAGACCACGCTCCCGTGTG
GACTCCGACGGCTCCTTCTTCTCTACAGCAAGCTCACCGTGACAAG
GACAGGTGGCAGCAGGGGAACGCTTCTCATGCTCCGTGATGCATGA
GGCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGG
TAAATGAGGATCCGTTAAACGTTACCAACTACCTAGACTGGATTCGT
ACAACATGCGGCCGTGATATCTACGTATGATCAGCCTCGACTGTGCT
TCTAGTTGCCAGCCATCTGTTGTTGCCCCCTCCCCGTCTTCTTGA
CCCTGGAAGGTGCCACTCCCACTGTCTTTTCTAATAAAATGAGGAAA
TTGCATCGCATTGTCTGAGTAGGTGTCTATTCTATTCGGGGGTGGGG
TGGGGCAGGACAGCAAGGGGGAGGATTGGGAAGACAATAGCAGGCA
TGCTGGGGATGCGGTGGGCTCTATGGAACAGCTGGGGCTCGACAGC
GCTGGATCTCCCGATCCCCAGCTTGTCTTCTCAATTTCTTATTGCTA
ATGAGAAAAAAGGAAAAATTAATTTTAAACCAATTCAGTAGTTGAT
TGAGCAAATGCGTTGCCAAAAAGGATGCTTTAGAGACAGTGTCTCT
GCACAGATAAGGACAAACATTATTCAGAGGGAGTACCCAGAGCTGAG
ACTCCTAAGCCAGTGAGTGGCAGCATTCTAGGGAGAAATATGCTT
GTATCAACCGAAGCCTGATTCGGTAGAGCCACACCTTGTGTAAGGGCC
ATACTGCTCACACAGGATAGAGAGGGCAGGAGCCAGGGCAGAGCAT
ATAAGGTGAGGTAGGATCAGTTGCTCCTCACATTTGCTTCTGACATAG
TTGTGTTGGGAGCTTGGATAGCTTGGACAGCTCAGG

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FIG. 84B

CAAAATCAACGGGACTTTCCAAAATGTCGTAACAACCTCCGCCCCATTG
ACGCAAATGGGCGGTAGGCGGTACGGTGGGAGGTCTATATAAGCAG
AGCTGGGTACGTCCTCACATTACGTGATCAGCACTGAACACAGACCC
GTCGACATGGGTTGGAGCCTCATCTTGCTCTTCCCTTGTCGCTGTTGCTA
CGCGTGTGCTAGCACCAAGGGCCCATCGGTCTTCCCCCTGGCACCCCT
CCTCCAAGAGCACCTCTGGGGGCACAGCGGCCCTGGGCTGCCTGGTC
AAGGACTACTTCCCCGAACCGGTGACGGTGTGCTGGAATCAGGCGC
CCTGACCAGCGGCGTGCACACCTTCCCGGCTGTCTACAGTCTCAGG
ACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTGGG
CACCCAGACCTACATCTGCAACGTGAATCACAAGCCCAAGCAACACCA
AGGTGGACAAGAAAGCAGAGCCCAAATCTTGTGACAAAACCTCACACA
TGCCCAACCGTGCCAGCACCTGAACTCCTGGGGGGACCGTCAGTCTTC
CTCTTCCCCCCTAAAACCAAGGACACCCCTCATGATCTCCCGGACCCCT
GAGGTCACTGCGTGGTGGTGGACGTGAGCCACGAAGACCCCTGAGGT
CAAGTTCACCTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGA
CAAAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGC
GTCTTACCGTCTCTGCACCAGGACTGGCTGAATGGCAAGGACTACAA
GTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCATCGAGAAAACCA
TCTCCAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCCTG
CCCCATCCCCGGGATGAGCTGACCAGGAACAGGTGACCGTGCACCTG
CCTGGTCAAAAGCCTTCTATCCAGCGACATCGCCGTGGAGTGGGAGA
GCAATGGGCAGCCGGAGAACAACCTACAAGACACGCCTCCCGTGCTG
GACTCCGACGGCTCCTTCTTCTCTACAGCAAGCTCACCGTGGACAAG
AGCAGGTGGCAGCAGGGGAACGTCTTCTCATGTCTCCGTGATGCATGA
GGCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGG
TAAATGAGGATCCGTTAACGGTTACCAACTACCTAGTATGGATTCCGTG
ACAACATGCGCGCGTGATATCTACGTATGATCAGCCTCGACTGTGCCT
TCTAGTTGCCAGCCATCTGTTGTTTGCCCCCTCCCCCGTGCCCTCCTTGA
CCCTGGAAGGTGCCACTCCCACTGTCTTTCCTAATAAAATGAGGAAA
TTGCATCGCATTGTCTGAGTAGGTGTCATTCTATTCTGGGGGGTGGGG
TGGGGCAGGACAGCAAGGGGGAGGATTGGGAAGACAATAGCAGGCA
TGCTGGGGATGCGGTGGGCTCTATGGAACCACTGGGGCTCGACAGC
GCTGGATCTCCCGATCCCCAGCTTTGCTTCTCAATTTCTTATTTGCATA
ATGAGAAAAAAAGGAAAAATTAATTTTAACACCAATTACAGTAGTTGAT
TGAGCAAATGCGTTGCCAAAAAGGATGCTTTAGAGACAGTGTTCTCT
GCACAGATAAGGACAAACATTATTCAGAGGGAGTACCCAGAGCTGAG
ACTCCTAAGCCAGTGAGTGGCACAGCATTCTAGGGAGAAATATGCTT
GTCTACCGCAAGCCTGATTCCGTAGAGCCACACCTTGGTAAAGGCC
AATCTGCTCACACAGGATAGAGAGGGCAGGAGCCAGGGCAGAGCAT
ATAAGGTGAGGTAGGATCAGTTGCTCCTCACATTTGCTTCTGACATAG
TTGTGTTGGGAGCTTGGATAGCTTGGACAGCTCAGG

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FIG. 84C

GCTGCGATTTCGCGCCAAAACCTTGACGGCAATCCTAGCGTGAAGGCTG
GTAGGATTTTATCCCCGCTGCCATCATGGTTCGACCATTGAACTGCAT
CGTCGCCGTGTCCCAAAATATGGGGATTGGCAAGAACGGAGACCTAC
CCTGGCCTCCGCTCAGGAACGAGTTCAAGTACTTCCAAAGAATGACC
ACAACCTCTTCAGTGGAAGGTAAACAGAAATCTGGTGATTATGGGTAG
GAAAACCTGGTTCTCCATTCTCGAGAACAATCGACCTTTAAAGGACA
GAATTAATATAGTTCTCAGTAGAGAACTCAAAGAACCACCACGAGGA
GCTCATTTTCTTGCCAAAAGTTTGGATGATGCCTTAAGACTTATTGAA
CAACCGGAATTGGCAAGTAAAGTAGACATGGTTTGGATAGTCGGAGG
CAGTTCTGTTTACCAGGAAGCCATGAATCAACCAGGCCACCTTAGACT
CTTTGTGACAAGGATCATGCAGGAATTTGAAAGTGACACGTTTTTCCC
AGAAATTGATTTGGGGAAATATAAACTTCTCCCAGAATACCCAGGCG
TCCTCTCTGAGGTCCAGGAGGAAAAAGGCATCAAGTATAAGTTTGAA
GTCTACGAGAAGAAAGACTAACAGGAAGATGCTTTCAGTTCTCTGC
TCCCCCTCTAAAGTCAATGCATTTTTTATAAGACCATGGGACTTTTGCTG
GCTTTAGATCAGCCTCGACTGTGCCTTCTAGTTGCCAGCCATCTGTTGT
TTGCCCTCCCCCGTGCCTTCCCTTGACCTGGAAGGTGCCACTCCCAC
TGTCCTTTCCTAATAAAATGAGGAAATTGCATCGCATTGTCTGAGTAG
GTGTCACTTCTATTCTGGGGGGTGGGGTGGGGCAGGACAGCAAGGGGG
AGGATTGGGAAGACATAAGCAGGCATGTGCGGATGCGGTGGGCTCT
ATGGAACCAGCTGGGGCTCGAGCTACTAGCTTTGCTTCTCAATTCTT
ATTTGCATAATGAGAAAAAAGGAAAAATTAATTTAACACCAATTCA
GTAGTTGATTGAGCAAATGCGTTGCCAAAAAGGATGCTTTAGAGACA
GTGTTCTCTGCACAGATAAGGACAAACATTATTCAGAGGGAGTACCC
AGAGCTGAGACTCTAAGCCAGTGAGTGGCAGCAGCATTCTAGGGAGA
AATATGCTTGTATCACCGAAGCCTGATTCCGTAGAGCCACACCTTGG
TAAGGGCCAATCTGCTCACACAGGATAGAGAGGGCAGGAGCCAGGG
CAGAGCATATAAGGTGAGGTAGGATCAGTTGCTCCTCACATTTGCTC
TGACATAGTTGTGTTGGGAGCTTGGATCGATCCTCTATGGTTGAACAA
GATGGATTGCACGCAGGTTCTCCGGCCGCTTGGGTGGAGAGGCTATT
GGCTATGACTGGGCACAACAGACAATCGGCTGCTCTGATGCCGCCGT
GTTCCGGCTGTGTCAGCGCAGGGGCGCCCGGTTCTTTTTGTCAAGACCGA
CCTGTCCGGTGCCCTGAATGAACTGCAGGACGAGGCAGCGCGGCTAT
CGTGGCTGGCCACGACGGGCGTTCCTTGCGCAGCTGATGCTCGACGTTG
TCACTGAAGCGGGAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGG
CAGGATCTCCTGTCTATCTCACCTTGCTCCTGCCAGAAAGTATCCATC
ATGGCTGATGCAATGCGGCGGCTGCATACGCTTGATCCGGCTACCTGC
CCATTGACACCAAGCGAAACATCGCATCGAGCGAGCAGTACTCG
GATGGAAGCCGGTCTTGTGTCATCAGGATGATCTGGACGAAGAGCATC
AGGGGCTCGCGCCAGCCGAACCTGTTGCCAGGCTCAAGGCGCGCATG
CCCCACGGCGAGGATCTCGTCGTGACCCATGGCGATGCCTGCTTGCCG

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FIG. 84D

AATATCATGGTGGAAAAATGGCCGCTTTTCTGGATTTCATCGACTGTGGC
CGGCTGGGTGTGGCGGACCGCTATCAGGACATAGCGTTGGCTACCCG
TGATATTGCTGAAAGAGCTTGGCGGCGAATGGGCTGACCGCTTCTCGT
GCTTTACGGTATCGCCGCTTCCCGATTTCGACGCGCATCGCCTTCTATC
GCCTTCTTGACGAGTTCTTCTGAGCGGGACTCTGGGGTTCGAAATGAC
CGACCAAGCGACGCCAACCTGCCATCAGGAGATTTCGATTCCACCG
CCGCTTCTATGAAAGGTGGGCTTCGGAATCGTTTCCGGGACGCCG
GCTGGATGATCCTCCAGCGCGGGGATCTCATGCTGGAGTTCTTCGCCC
ACCCCAACTTGTTTATTGACGCTTATAATGGTTACAAATAAAGCAATA
GCATCACAAATTTACAAATAAAGCATTTTTTCACTGCATTCTAGTT
GTGGTTTGTCCAAATCATCAATCTATCTTATCATGTCTGGATCGCGG
CCGCGATCCCGTCGAGAGCTTGGCGTAATCATGGTCATAGCTGTTTCC
TGTTGAAATTGTTATCCGCTCACAATCCACACAACATACGAGCCGG
AGCATAAAGTGTAAGCCCTGGGGTGCCTAATGAGTGAGCTAACTCAC
ATTAATTGCGTTGCGCTCACTGCCGCTTTCAGTCGGGAAACCTGTC
GTGCCAGCTGCATTAATGAATCGGCCAACGCGGGGAGAGCGGTT
TGCGTATTGGGCGCTCTCCGCTTCCCTCGCTCACTGACTCGCTGCGCTC
GGTCGTTGCGCTGCGGCGAGCGGTATCAGCTCACTCAAAGGCGGTAA
TACGTTTATCCACAGAATCAGGGGATAACGCAGGAAAGAACATGTGA
GCAAAAGGCCAGCAAAAGGCCAGGAACCGTAAAAAGGCCGCGTTGC
TGCGTTTTTCCATAGGCTCCGCCCTGACGAGCATCACAAAAATC
GACGCTCAAGTCAGAGGTGGCGAAACCGACAGGACTATAAAGATAC
CAGGCGTTTTCCCTGGAAGCTCCCTCGTGCGCTCTCCTGTTCCGACC
CTGCCGCTTACCGGATACCTGTCCGCTTTCTCCCTTCGGGAAGCGTG
GCGCTTTCTCAATGCTACGCTGTAGGTATCTCAGTTCCGTTAGGTC
GTTCTGCTCAAAGCTGGGCTGTGTGCACGAACCCCGTTACGCCGAC
CGCTGCGCTTATCCGGTAACTATCGTCTTGAGTCCAACCCGGTAAGA
CACGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATTAGCAG
AGCGAGGTATGTAGGCGGTGCTACAGAGTTCTTGAAGTGGTGGCTA
ACTACGGCTACACTAGAAAGACAGTATTTGGTATCTGCGCTTGCTGA
AGCCAGTTACCTTCGGAAAAAGAGTTGGTAGCTCTTGATCCGGCAAA
CAAACCACCGTGGTAGCGGTGGTTTTTTTGTGTTGCAAGCAGCAGATT
ACGCGCAGAAAAAAGGATCTCAAGAAGATCCTTTGATCTTTTCTAC
GGGGTCTGACGCTCAGTGGAACGAAAACTACGTTAAGGGATTTTGG
TCATGAGATTATCAAAAAAGGATCTTACCTAGATGCTTTTAAATAAA
AATGAAGTTTAAATCAATCTAAAGTATATAGCTAAACCTGGTCTG
ACAGTTACCAATGCTTAATCAGTGAGGCACCTATCTCAGCGATCTGTC
TATTTCTGTTTCATCCATAGTTGCCTGACTCCCCGTCGTGTAGATAACTAC
GATACGGGAGGGCTTACCATCTGGCCCCAGTGCTGCAATGATACCGC
GAGACCAACGCTCACCAGCTCCAGATTTATCAGCAATAAACCAAGCCA
GCCGGAAGGGCCGAGCGCAGAGTGGTCCGCAACTTTATCCGCCTC
CATCCAGTCTATTAATTGTTGCCGGGAAGCTAGAGTAAAGTAGTTCGC

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FIG. 84E

CAGTTAATAGTTTGC GCAACGTTGTTGCCATTGCTACAGGCATCGTGG
TGTCACGCTCGTTCGTTTGGTATGGCTTCATTCAGCTCCGGTTCCCAAC
GATCAAGGCGAGTTACATGATCCCCATGTTGTGCAAAAAAGCGGTT
AGCTCCTTCGGTCCCTCCGATCGTTGTCAGAAAGTAAGTTGGCCGCGAGTG
TTATCACTCATGGTTATGGCAGCACTGCATAATTCTCTTACTGTCAATGC
CATCCGTAAGATGCTTTTCTGTGACTGGTGAGTACTCAACCAAGTCAT
TCTGAGAATAGTGTATGCGGCGACCGAGTTGCTCTTGCCCGGCGTCAA
TACGGGATAATACCGCGCCACATAGCAGAACTTTAAAAGTGCTCATC
ATTGGAAAACGTTCTTCGGGGCGAAAACCTCTCAAGGATCTTACCGCTG
TTGAGATCCAGTTCGATGTAACCCACTCGTGCACCCAAGTATCTTCA
GCATCTTTTACTTTTACCAGCGTTTCTGGGTGAGCAAAAAACAGGAAGG
CAAAATGCCGCAAAAAAGGGAATAAGGGCGACACGGAAATGTTGAA
TACTCATACTCTTCCTTTTTCAATATTATTGAAGCATTTATCAGGGTTA
TTGTCTCATGAGCGGATACATATTTGAATGTATTTAGAAAAATAAACA
AATAGGGGTTCCGCGCACATTTCCCCGAAAAGTGCCACCT

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FIG. 85A

GACGTCGCGGCCGCTCTAGGCCCTCCAAAAAGCCTCCTCACTACTTCT
GGAATAGCTCAGAGGCCGAGGCGGCCCTCGGCCCTCTGCATAAAATAAA
AAAATTAGTCAGCCATGCATGGGGCGGAGAATGGGCGGAAGTGGGGCG
GAGTTAGGGGCGGGATGGGCGGAGTTAGGGGCGGGACTATGGTTGCT
GACTAATTGAGATGCATGCTTTGCATACTTCTGCCTGCTGGGGAGCCT
GGGGACTTTCCACACCTGGTTGCTGACTAATTGAGATGCATGCTTTGC
ATACTTCTGCCTGCTGGGGAGCCTGGGGACTTTCCACACCCTAACTGA
CACACATTCCACAGAATTAATTCCCCTAGTTATTAATAGTAATCAATT
ACGGGGTCATTAGTTCATAGCCCATATATGGAGTTCCGCGTTACATAA
CTTACGGTAAATGGCCCGCCTGGCTGACCGCCCAACGACCCCCGCC
ATTGACGTCAATAATGACGTATGTTCCCATAGTAACGCCAATAGGGA
CTTTCCATTGACGTCAATGGGTGGACTATTTACGGTAAACTGCCACT
TGGCAGTACATCAAGTGTATCATATGCCAAGTACGCCCTTATTGAG
TCAATGACGGTAAATGGCCCGCCTGGCATTATGCCAGTACATGACCT
TATGGGACTTTTCTACTTGGCAGTACATCTACGTATTAGTCATCGCTA
TTACCATGGTGATGCGGTTTTTGGCAGTACATCAATGGGCGTGGATACC
GGTTTGACTCACGCGGATTTCCAAGTCTCCACCCATTGACGTCAATG
GGAGTTTGTTTTGGCACCAAAATCAACGGGACTTTCCAAAAATGTCGTA
ACAACTCCGCCCCATTGACGCAAAATGGGCGGTAGGCGTGTACGGTGG
GAGAGCCCATCAGCAGATCTCTCACTATGGATTTTCAGGTGCAGATTAT
CAGCTTCTTGCTAATCAGTGCTTCAGTCATAATGTCCAGAGGACAAAT
TGTTCTCTCCAGTCTCCAGCAATCCTGTCTGCATCTCCAGGGGAGAA
GGTCACAATGACTTGCAGGGCCAGCTCAAGTGTAAGTTACATCCACT
GGTTCAGCAGAAGCCAGGATCCTCCCCCAAACCCCTGGATTTATGCCA
CATCCAACCTGGCTTCTGGAGTCCCTGTTCTCAGTGGCAGTGGGT
CTGGGACTTCTTACTCTCTCACAATCAGCAGAGTGGAGGCTGAAGATG
CTGCCACTTATTACTGCCAGCAGTGGACTAGTAACCCACCCACGTTTCG
GAGGGGGGACCAAGCTGGAAATCAAACGTACGGTGGCTGCACCATCT
GTCTTCATCTTCCCGCCATCTGATGAGCAGTTGAAATCTGGAAGTCC
CAGTGGAAGGTGGATAACGCCCTCCAATCGGGTAACTCCAGGAGAG
TGTCACAGAGCAGACAGCAAGGACAGCACCTACAGCCTCAGCAGCA
CCCTGACGCTGAGCAAAGCAGACTACGAGAAACACAAAGTCTACGCC
TGCGAAGTCACCCATCAGGGCCTGAGCTCGCCCGTCACAAAGAGCTT
CAACAGGGGAGAGTGTTGAATTCAGATCCGTTAACGGTTACCAACTA
CCTAGACTGGATTTCGTGACAACATGCGGCCGTGATATCTACGTATGAT
CAGCCTCGACTGTGCCCTTCTAGTTGCCAGCCATCTGTTGTTTGCCCTC
CCCCGTGCCCTTCCTTGACCCCTGGAAGGTGCCACTCCCACTGTCCTTCC

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FIG. 85B

TATAAAAATGAGGAAATTGCATCGCATTGCTGAGTAGGTGTCATTCT
ATTCTGGGGGGTGGGGTGGGGCAGGACAGCAAGGGGGAGGATTGGG
AAGACAATAGCAGGCATGCTGGGGATGCGGTGGGCTCTATGGAACCA
GCTGGGGCTCGACAGCTATGCCAAGTACGCCCCCTATTGACGTC AATG
ACGGTAAATGGCCCCGCCTGGCATTATGCCAGTACATGACCTTATGGG
ACTTTCCTACTTGGCAGTACATCTACGTATTAGTCATCGCTATTACCAT
GGTGATGCGGTTTTGGCAGTACATCAATGGGCGTGATAGCGGTTTG
ACTCACGGGGATTTC AAGTCTCCACCCCATGACGTC AATGGGAGTT
TGTTTTGGCACAAAATCAACGGGACTTCCAAAATGTCGTAACAACCT
CCGCCCCATTGACGCAAAATGGGCGGTAGGCGTGTACGGTGGGAGGTC
TATATAAGCAGAGCTGGGTACGTCTCACAATTCAGTGATCAGCACTGA
ACACAGACCCGTCGACATGGGTTGGAGCCTCATCTTGCTCTTCCTTGT
CGCTGTTGCTACGCGTGTCTGTCCAGGTACAACCTGCAGCAGCCTGG
GGCTGAGCTGGTGAAGCCTGGGGCCTCAGTGAAGATGTCCTGCAAGG
CTTCTGGCTACACATTTACCAGTTACAATATGCACTGGGTAAAACAGA
CACCTGGTCGGGGCCTGGAATGGATTGGAGCTATTATCCCGGAAAT
GGTGATACTTCTACAATCAGAAGTTCAAAGGCAAGGCCACATTGAC
TGCAGACAAATCCTCCAGCACAGCCTACATGCAGCTCAGCAGCCTGA
CATCTGAGGACTCTGCGGTCTATTACTGTGCAAGATCGACTTACTACG
GCGGTGACTGGTACTTCAATGTCTGGGGCGCAGGACCACGGTCACC
GTCTCTGCAGCTAGCACCAAGGGCCCATCGGTCTTCCCCCTGGCACCC
TCTCCAAGAGCACCTCTGGGGGCACAGCGGCCCTGGGCTGCCTGGT
CAAGGACTACTTCCCCGAACCGGTGACGGTGTCTGTGGAACCTCAGGCG
CCCTGACCAGCGGCGTGCACACCTTCCCGGCTGTCTACAGTCCTCAG
GACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGCACTTGG
GCACCCAGACCTACATCTGCAACGTGAATCACAAGCCGACCAACACC
AAGGTGGACAAGAAAGCAGAGCCCAAATCTTTGTGACAAAACCTCACAC
ATGCCCCACCGTGCCAGCACCTGAACTCCTGGGGGGACCGTCAGTCTT
CCTCTTCCCCC A A A A C C C A A A G G A C A C C C T C A T G A T C T C C C G A C C C
TGAGGTACATGCGTGGTGGTGGACGTGAGCCACGAAGACCTTGAGG
TCAAGTTCAACTGTACGTGGAGCGGCTGGAGGTGCATAATGCCAAG
ACAAAGCCGCGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAG
CGTCTCACCGTCTGCAACCAGGACTGGCTGAATGGCAAGGAGTACA
AGTGCAAGGTCTCCAACAAAGCCCTCCAGCCCCCATCGAGAAAACC
ATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCAAGGTGATACACCT
GCCCCATCCCGGGATGAGCTGACCAAGAACCAGCAGCTGACACCT
GCCTGGTCAAAGGCTTCTATCCAGCGACATCGCCGTGGAGTGGGAG
AGCAATGGGCAGCCGGAGAACAACCTACAAGACCACGCCTCCCGTGCT
GGACTCCGACGGCTCCTTCTTCTCTACAGCAAGCTCACCGTGGACAA
GAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATG
AGGCTCTGCACAACCACTACACGCAGAAGAGCCTTCCCTGTCTCCGG
GTAATGAGGATCCGTTAACGGTTACCAACTACCTAGACTGGATTCTG

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FIG. 85C

GACAACATGCGGCCGTGATATCTACGTATGATCAGCCTCGACTGTGCC
TTCTAGTTGCGAGCCATCTGTTGTTTGCCCCCTCCCCCGTGCCTTCCTTG
ACCCCTGGAAGGTGCCACTCCCAGTGCCTTCTCAATAAAAATGAGGAA
ATTGCATCGCATTGCTGAGTAGGTGTCATTCTATTCTGGGGGGTGGG
GTGGGGCAGGACAGCAAGGGGGAGGATTGGGAAGACAATAGCAGGC
ATGCTGGGGATGCGGTGGGCTCTATGGAACAGCTGGGGCTCGACAG
CGCTGGATCTCCCGATCCCCAGCTTTGCTTCTCAATTTCTTATTGTCAT
AATGAGAAAAAAGGAAAAATTAATTTTAACACCAATTCAGTAGTTGA
TTAGCAAAATGCGTTGCCAAAAAGGATGCTTTAGAGACAGTGTCTCT
GCACAGATAAGGACAAACATTATTACAGAGGGAGTACCCAGAGCTGAG
ACTCCTAAGCCAGTGAGTGGCACAGCATTCTAGGGAGAAATATGCTT
GTCATCACCCGAAGCCTGATTCCGTAGAGCCACACCTTGTAAGGGCC
AATCTGCTCACACAGGATAGAGAGGGCAGGAGCCAGGCCAGAGCAT
ATAAGGTGAGGTAGGATCAGTTGCTCCTCACATTTGCTTCTGACATAG
TTGTGTTGGGAGCTTGATAGCTTGACAGCTCAGGGCTGCGATTTCG
CGCCAACTTGACGGCAATCCTAGCGTGAAGGCTGGTAGGATTTTATC
CCCGCTGCCATCATGGTTCGACCATTTGAACGATGCATCGTCGCCGTGTC
CAAAATATGGGATTGGCAAGAACGGAGACCTACCCCTGGCCTCCGCT
CAGGAACGAGTTCAAGTACTTCAAAGAATGACCACAACCTCTTCAG
TGGAAGGTAAACAGAATCTGGTGATTATGGGTAGGAAAAACCTGGTTC
TCCATTCTTGAGAAGAATCGACCTTTAAAGGACAGAATTAATATAGTT
CTCAGTAGAGAACTCAAAGAACCACACGAGGACTCATTTTCTTGTC
CAAAAGTTTGGATGATGCCCTTAAGACTTATTGAACAACCGGAATTGG
CAAGTAAAGTAGACATGGTTTGGATAGTCGGAGGCAGTTCTGTTTACC
AGGAAGCCATGAATCAACCAGGCCACCTTAGACTCTTTGTGACAAGG
ATCATGCAGGAATTTGAAAAGTGACACGTTTTTCCAGAAATTGATTG
GGGAAATATAAACTTCTCCAGAATACCCAGCGCTCTCTGAT
GGTCCAGGAGGAAAAAGGCATCAAGTATAAGTTTGAAGTCTACGAGA
AGAAAGACTAACAGGAAGATGCTTTCAAGTTCTCTGCTCCCTCCTAA
AGCTATGCATTTTATAAGACCATGGGACTTTTGCTGGCTTTAGATCA
GCCTCGACTGTGCCCTCTAGTTGCCAGCCATCTGTTGTTGCCCCCTCC
CCGTGCCCTTCTTGACCCCTGGAAGGTGCCACTCCCATTGCTCTTCTTA
ATAAAATGAGGAAATTGCATCGCATTGTCTGAGTAGGTGTCATTCTAT
TCTGGGGGGTGGGGTGGGGCAGGACAGCAAGGGGGAGGATTGGGAA
GACAATAGCAGGCATGCTGGGGATGCGGTGGGCTCTATGGAACCAGC
TGGGGCTCGAGCTACTAGCTTTGCTTCTCAATTTCTATTTCATTAATG
AGAAAAAAGGAAAAATTAATTTTAACACCAATTGATAGTTGATTGA
GCAAATGCGTTGCCAAAAAGGATGCTTTAGAGACAGTGTCTCTGCA
CAGATAAGGACAAACATTATTACAGAGGGAGTACCCAGAGCTGAGAG
CCTAAGCCAGTGAGTGGCACAGCATTCTAGGGAGAAATATGCTTGTC
ATCACCGAAGCCTGATTCCGTAGAGCCACACCTTGTAAGGGCCAAT
CTGCTCACACAGGATAGAGAGGGGCAGGAGCCAGGGCAGAGCATATA
AGGTGAGGTAGGATCAGTTGCTCCTCACATTTGCTTCTGACATAGTTG

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FIG. 85D

TGTTGGGAGCTTGGATCGATCCTCTATGGTTGAACAAGATGGATTGCA,
CGCAGGTTCTCCGGCCGCTTGGGTGGAGAGGCTATTCGGCTATGACTG
GGCACAACAGACAATCGGCTGCTCTGATGCCCGGTGTTCCGGCTGTC
AGCGCAGGGGCGCCCGGTTCTTTTTGTCAAGACCGACCTGTCCGGTGC
CCTGAATGAACTGCAGGACGAGGCAGCGCGGCTATCGTGGCTGGCCA
CGACGGGCGTTCTTGGCGAGCTGTGCTCGACGTTGTCACTGAAGCGG
GAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGGCAGGATCTCCTG
TCATCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCA
ATGCGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTCGACCAC
CAAGCGAAACATCGCATCGAGCGAGCACGTACTCGGATGGAAGCCGG
TCTTGTCGATCAGGATGATCTGGACGAAGAGCATCAGGGGCTCGCGC
CAGCCGAACGTTCGCCAGGCTCAAGGCGCGCATGCCGACGGCGAG
GATCTCGTCGTGACCCATGGCGATGCCTGCTTGCCGAATATCATGGTG
GAAAATGGCCGCTTTTCTGGATTTCAGCTGTGGCCGGCTGGGTGTG
GCGGACCGCTATCAGGACATAGCGTTGGCTAGCCGTTCTCTCGTGTTCACGGTAT
AGAGCTTGGCGGCGAATGGGCTGACCGCTTCTCTCGTGTTCACGGTAT
CGCCGCTCCCGATTTCGAGCGCATCGCCTTCTATCGCCTTCTTGACGA
GTTCTTCTGAGCGGGACTCTGGGGTTCGAAATGACCGACCAAGCGAC
GCCCAACCTGCCATCACGAGATTTCGATTCCACCGCCGCCTTCTATGA
AAGGTTGGGCTTCGGAATCGTTTTCCGGGACGCCGGCTGGATGATCCT
CCAGCGCGGGGATCTCATGTCTGGAGTTCTTCGCCACCCCACTTGT
TATTGCAGCTTATAAATGGTTACAAATAAAGCAATAGCATCACAAATTT
CACAAATAAAGCATTTTTTTTCACTGCATTCTAGTTGTGGTTTGTCCAA
ACTCATCAATCTATCTTATCATGTCTGGATCGCGGCCGCGATCCCGTC
GAGAGCTTGGCGTAATCATGGTCATAGCTGTTTCTGTGTGAAATTTG
TATCCGCTCACAAATTCACACAACATACGAGCCGGAAGCATAAAGTG
TAAAGCTTGGGTGCCTAATGAGTGAGCTAACTACATTAATTCGGTT
TCGCTACTGCCCCGCTTTCCAGTCGGGAAACCTGTCTGTGCCAGCTGCA
TTAATGAATCGGCCAACGCGCGGGGAGAGGCGGTTTGCCTATTGGGC
GCTCTTCCGCTTCTCTGCTCACTGACTCGCTGCGCTCGGTGCTTCGGCT
GCGGCGAGCGGTATCAGCTCACTCAAAGGCGGTAATACGGTTATCCA
CAGAATCAGGGGATAACGCAGGAAAGAATGTGAGCAAAAGGCCA
GCAAAAGGCCAGGAACCGTAAAAAGGCCGCGTGTGCTGGCGTTTTC
ATAGGCTCCGCCCCCTTACGAGCATCACAAAAATCGACGCTCAAGT
CAGAGGTGGCGAAACCCGACAGGACTATAAAGATACCAGGCGTTTCC
CCCTGGAAGCTCCCTCGTGCCTCTCTGTTCCGACCTGCGCGTTAC
CGGATACCTGTCCGCTTTCTCCCTTCGGGAAGCGTGGCGCTTTCTCA
ATGCTCACGCTGTAGGTATCTCAGTTCCGGTGTAGGTGCTTCGCTCCAA
GCTGGGCTGTGTGCACGAACCCCCGTTACGCCGACCGCTGCGCCTT
ATCCGGTAACATATCGTCTTGAGTCCAACCCGGTAAGACACGACTTATC

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FIG. 53A

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ACTTTTAAATTTAATGTATAGAATAGAGATATACATAGGATATGTAA
TAGATACACAGTGTATATGTGATTAAAAATATAATGGGAGATTCAATC
AGAAAAAAGTTTCTAAAAAGGCTCTGGGGTAAAAGAGGAAGGAAAC
AATAATGAAAAAAATGTGGTGAGAAAAACAGCTGAAAACCCATGTA
AAGAGTGTATAAAGAAAAGCAAAAAGAGAAAGTAGAAAAGTAACACAGG
GGCATTGGAAAAATGTAAACGAGTATGTTCCCTATTTAAGGCTAGGC
ACAAAGCAAGGTCTTCAGAGAACCTGGAGCCTAAGGTTTAGGCTCAC
CCATTTCAACCAGTCTAGCAGCATCTGCAACATCTACAATGGCCTTGA
CCTTTGCTTTACTGGTGGCCCTCCTGGTGCTCAGCTGCAAGTCAAGCT
GCTCTGTGGGCTGTGATCTGCCTCAAACCCACAGCCTGGGTAGCAGG
AGGACCTTGATGCTCCTGGCACAGATGAGGAGAAATCTCTCTTTCTCC
TGCTTGAAGGACAGACATGACTTTGGATTTCCCGAGGAGGAGTTTG
CAACCAGTTCCAAAAGGCTGAAACCATCCCTGTCCTCCATGAGATGA
TCCAGCAGATCTTCAATCTCTTCAGCACAAAGGACTCATCTGCTGCTT
GGGATGAGACCCTCCTAGACAAATTCTACACTGAACTCTACCAGCAG
CTGAATGACCTGGAAGCCTGTGTGATACAGGGGGTGGGGGTGACAG
GACTCCCCTGATGAAGGAGGACTCCATTCTGGCTGTGAGGAAATACT
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ACAAACTTGCAAGAAAGTTTAAAGAAGTAAGGAATGAAAACCTGGTTCA
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ATCTGCCATTTCAAAGACTCATGTTTCTGCTATGACCATGACACGATT
TAAATCTTTTCAAATGTTTTTAGGAGTATTAATCAACATTGTATTAG
CTCTTAAGGCACTAGTCCCTTACAGAGGACCATTGCTGACTGATCCATT
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ATGAAGAGAAGAAGGAACG

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FIG. 85E

GCCACTGGCAGCAGCCACTGGTAACAGGATTAGCAGAGCGAGGTATG
TAGGCGGTGCTACAGAGTTCCTGAAGTGGTGGCCTAACTACGGCTAC
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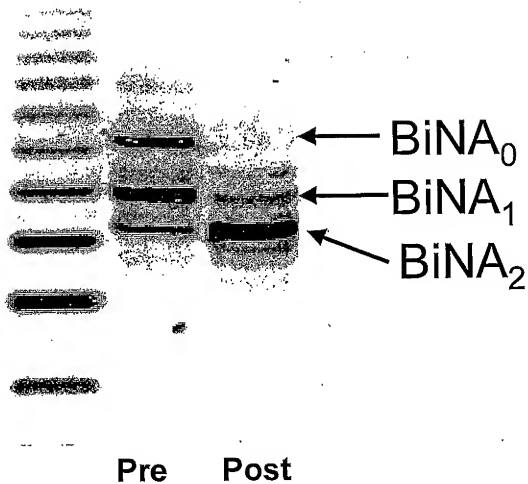


FIG. 86

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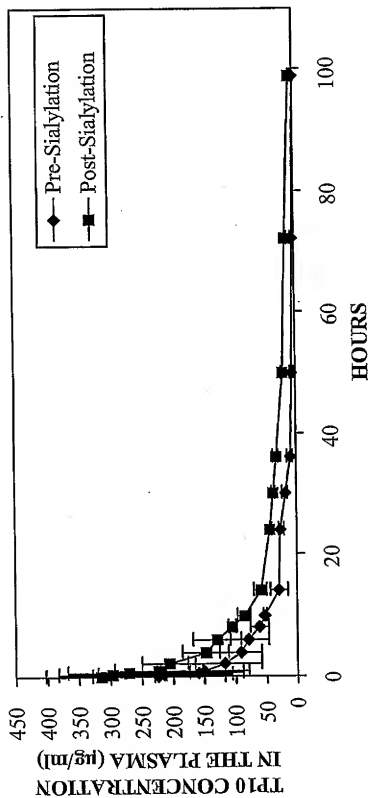


FIG. 87

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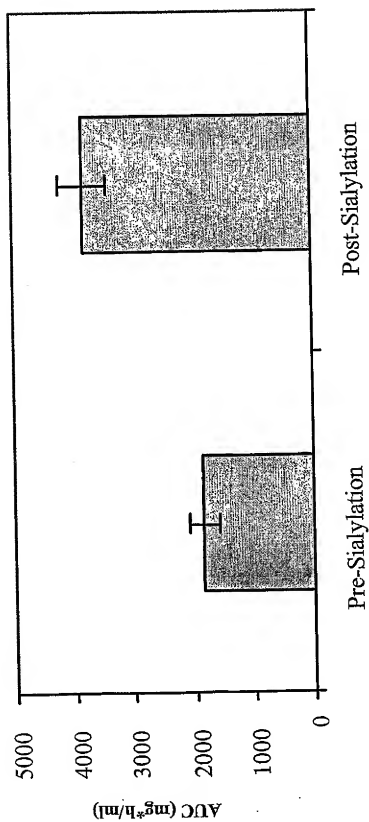


FIG. 88

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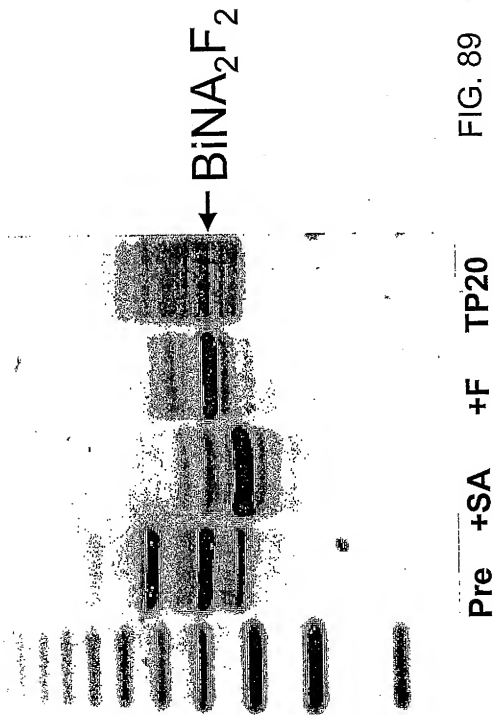


FIG. 89

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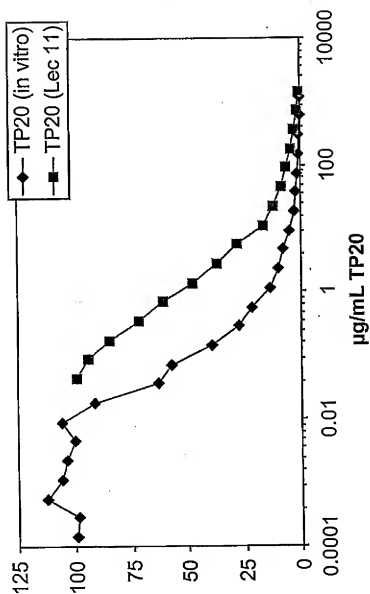


FIG. 90

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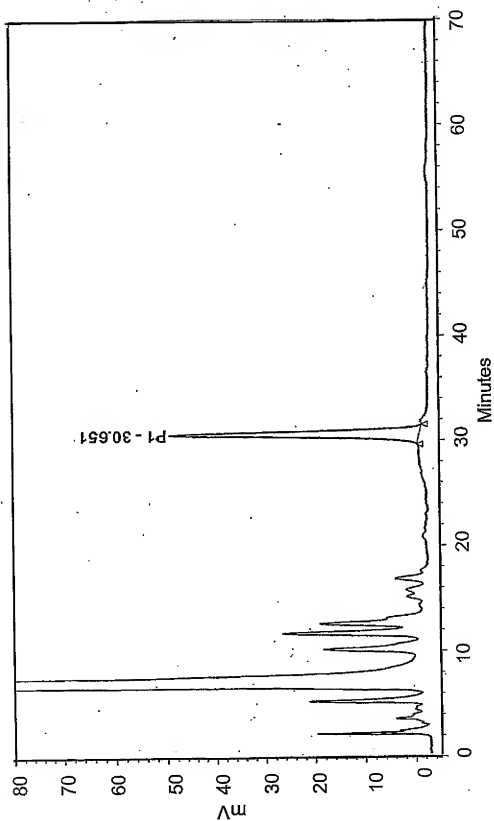


FIG. 91

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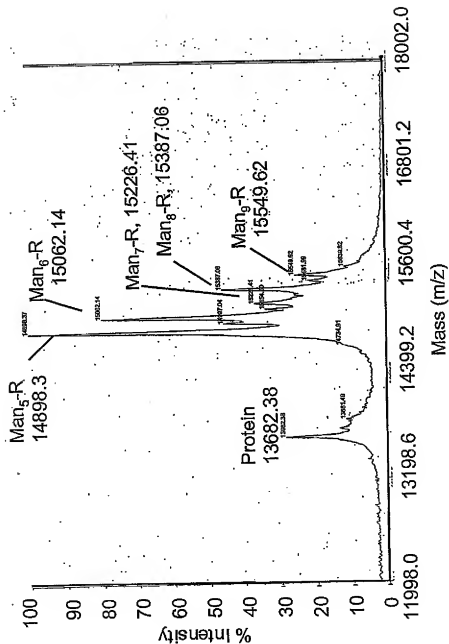


FIG. 92A

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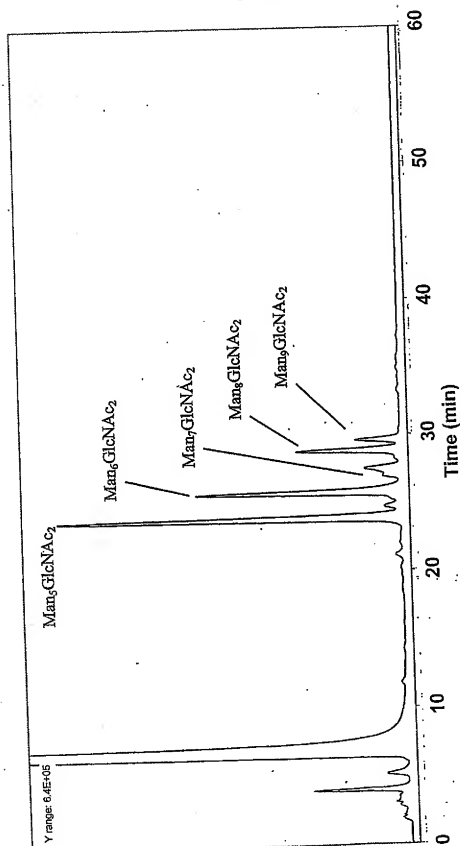


FIG. 92B

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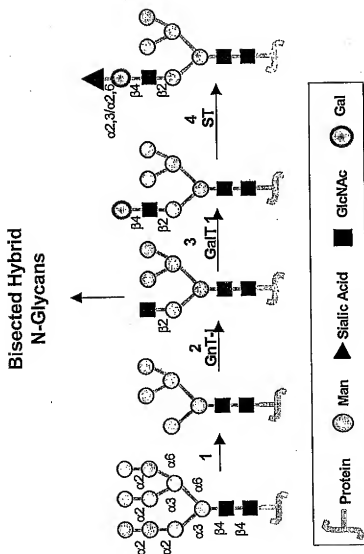
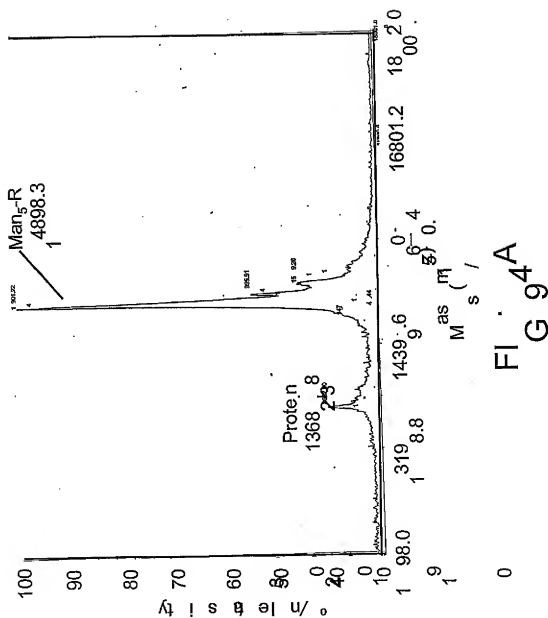
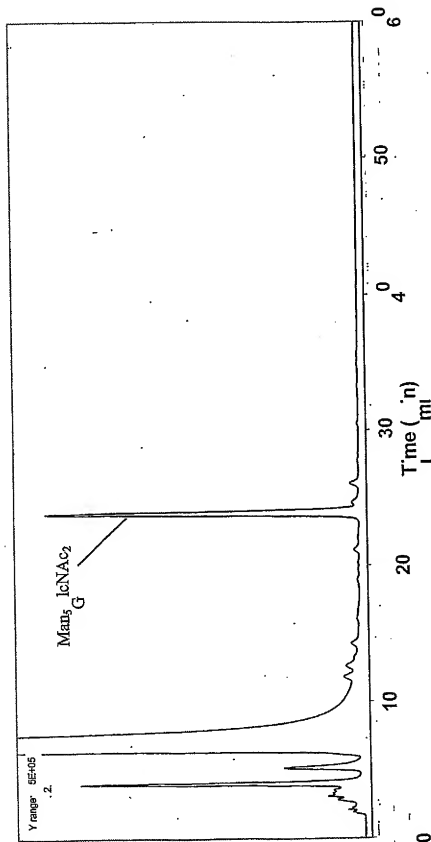


FIG. 93

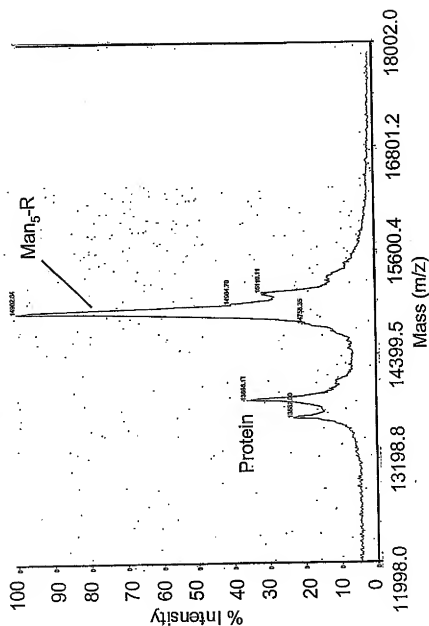
310/345



311/345

F 94B
IG.

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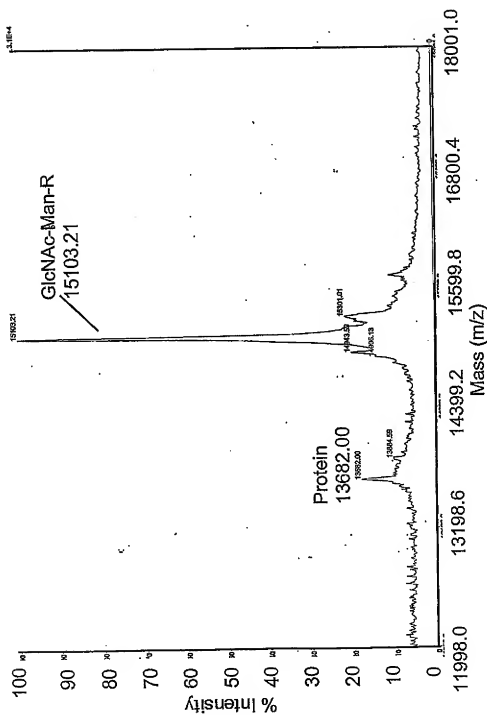


FIG. 96

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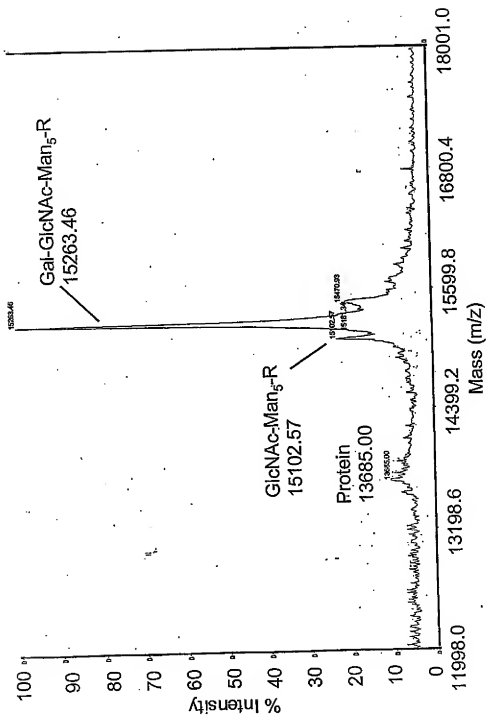
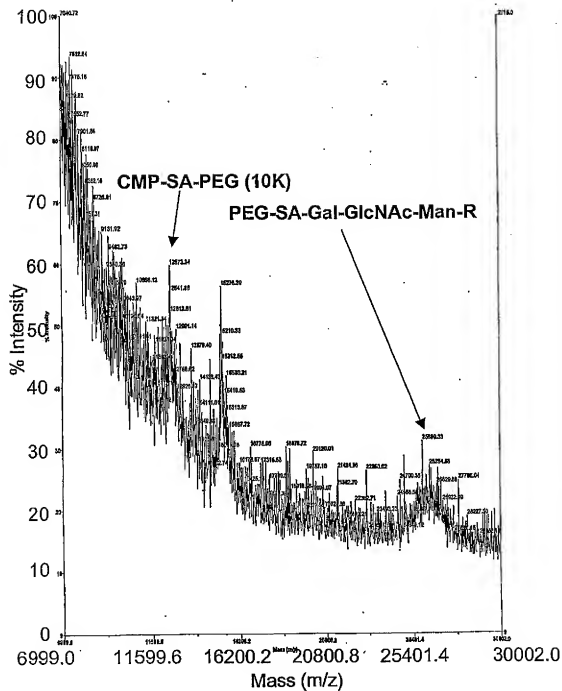


FIG. 97

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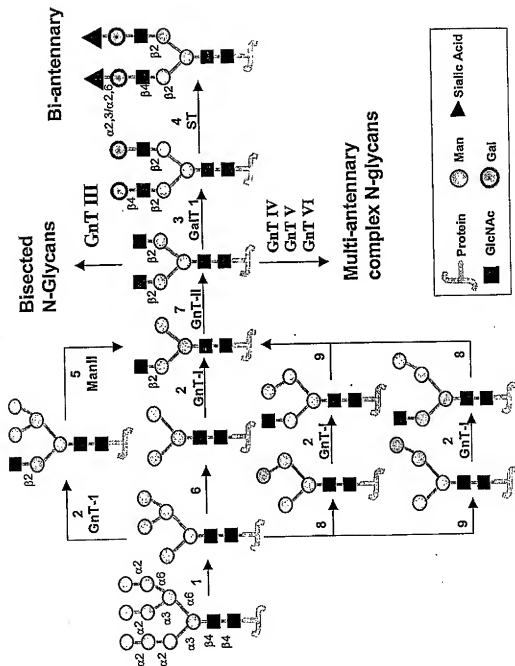


FIG. 100

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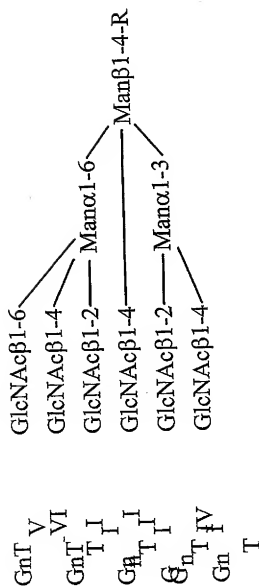


FIG. 101

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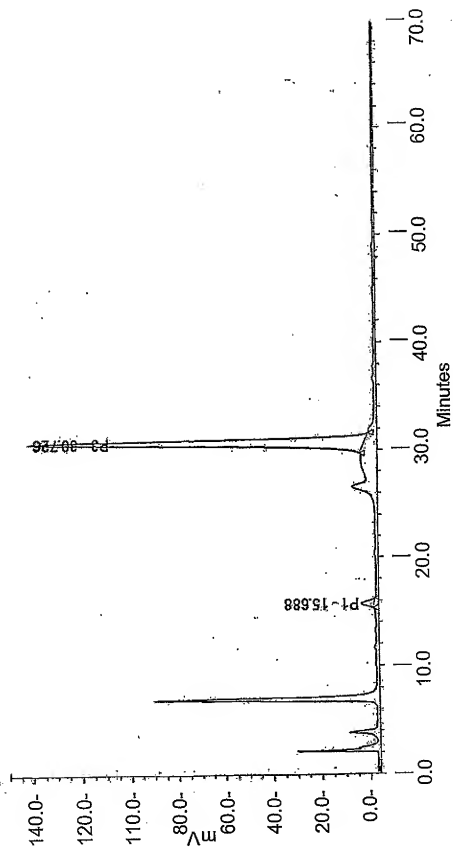


FIG. 102A

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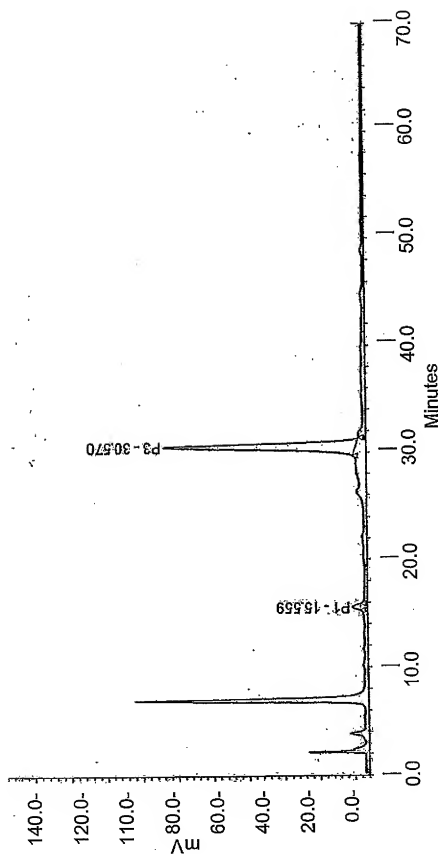


FIG. 102B

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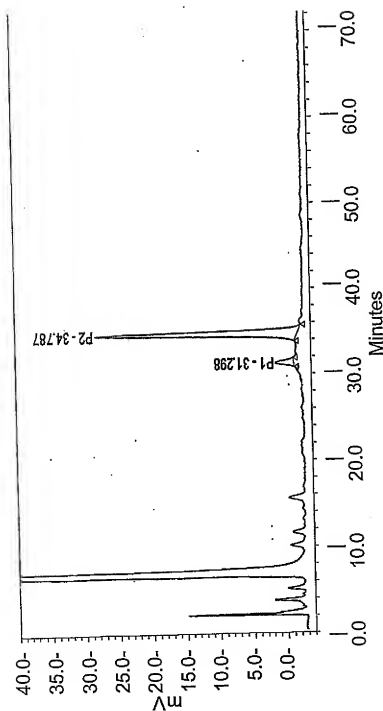


FIG. 103

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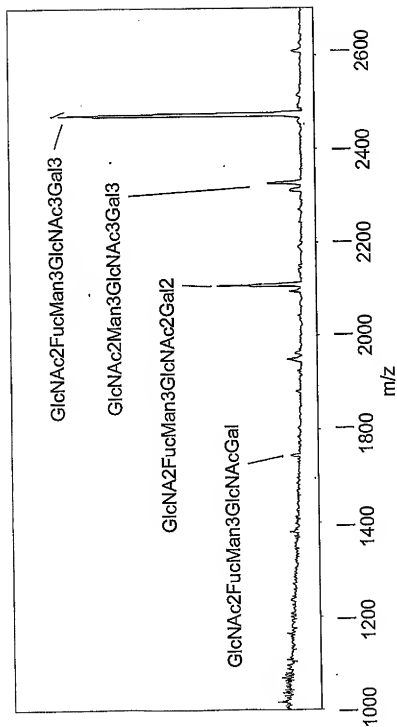


FIG. 104

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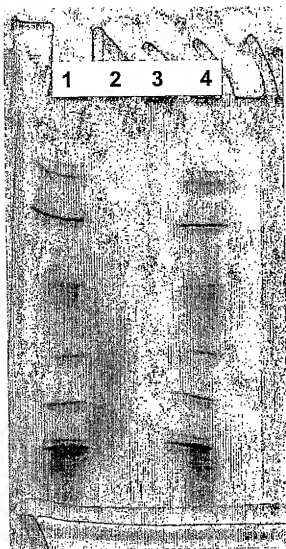


FIG. 105

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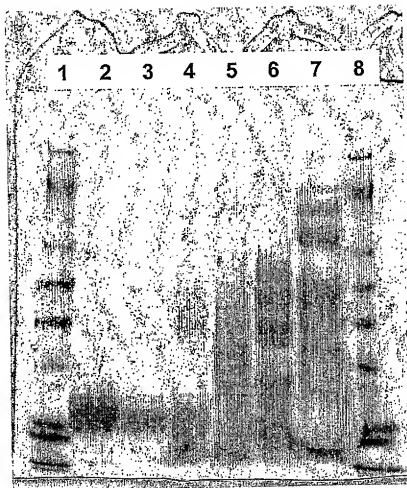


FIG. 106

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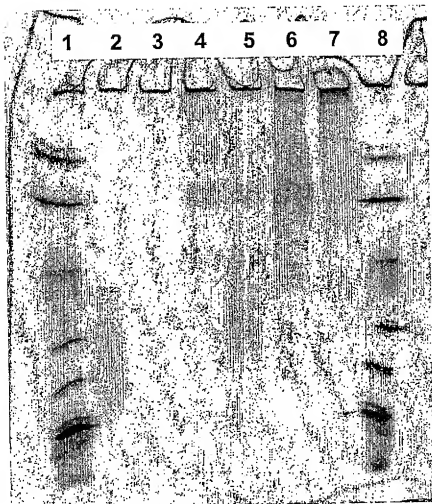


FIG. 107

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FIG. 108

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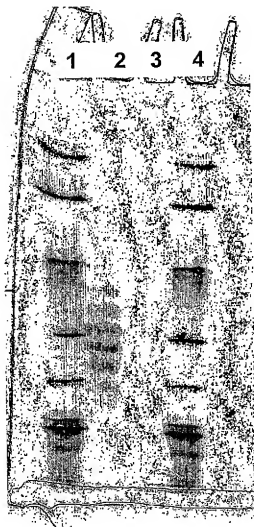


FIG. 109

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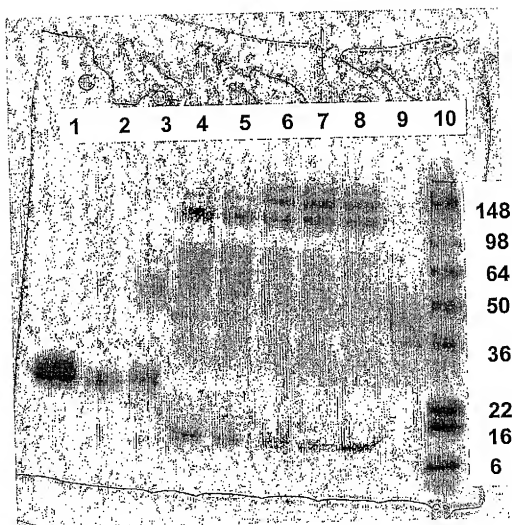


FIG. 110

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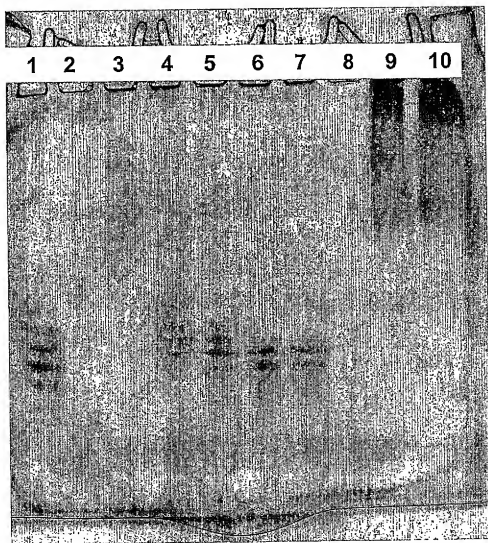


FIG. 111

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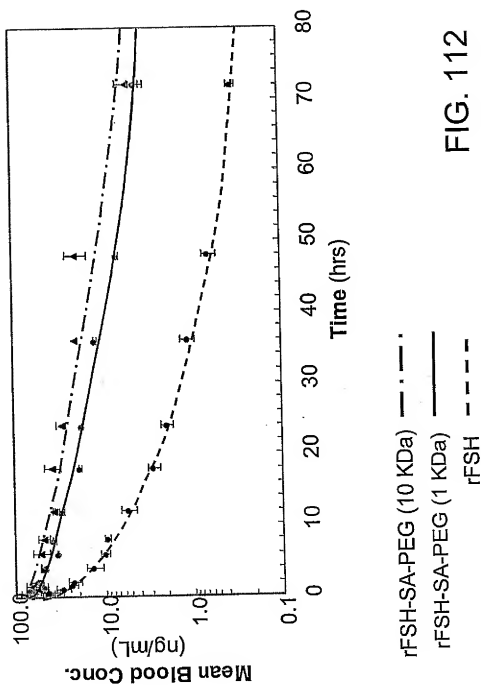


FIG. 112

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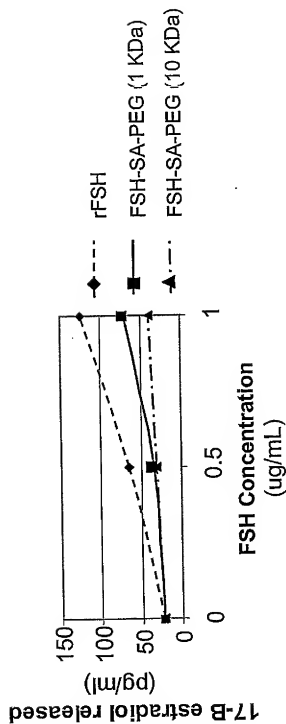


FIG. 113

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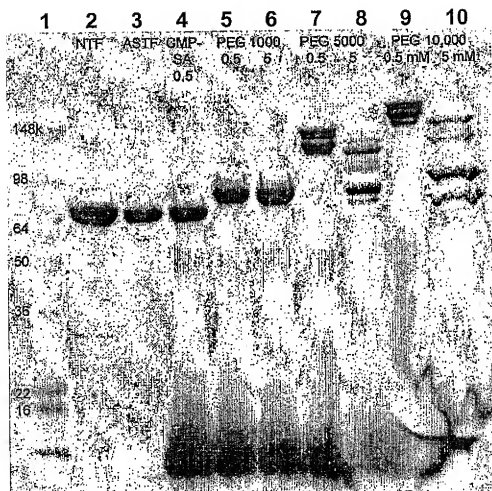


FIG. 114

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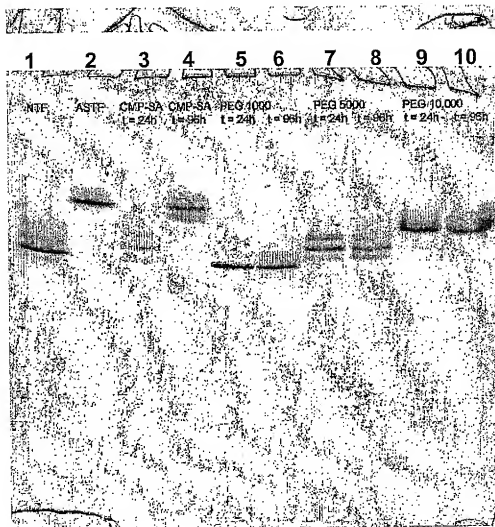


FIG. 115

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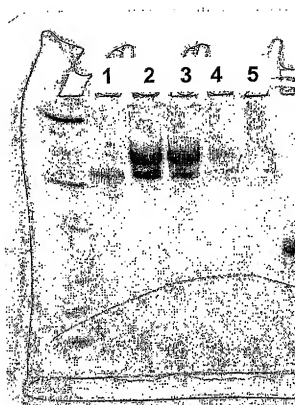


FIG. 116

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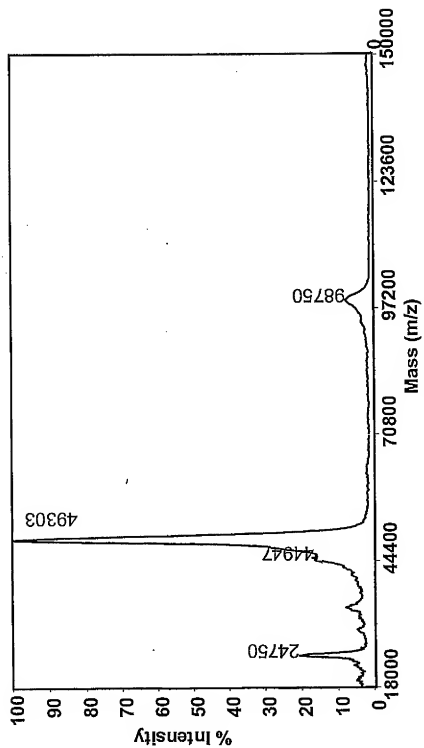


FIG. 117

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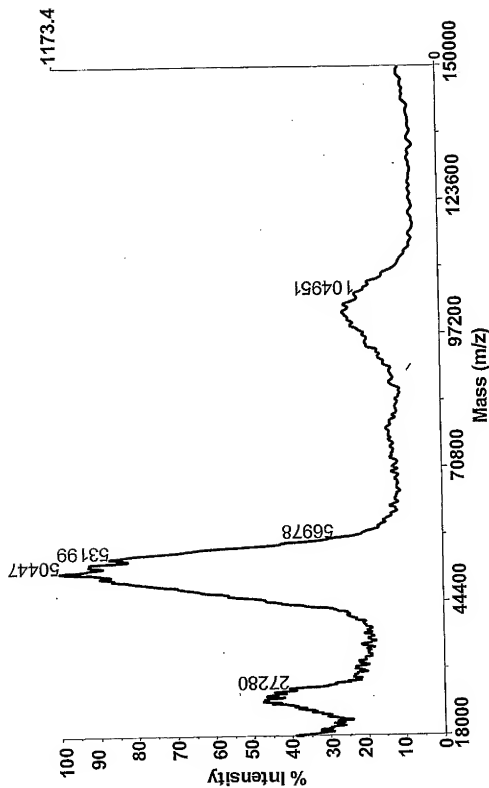


FIG. 118

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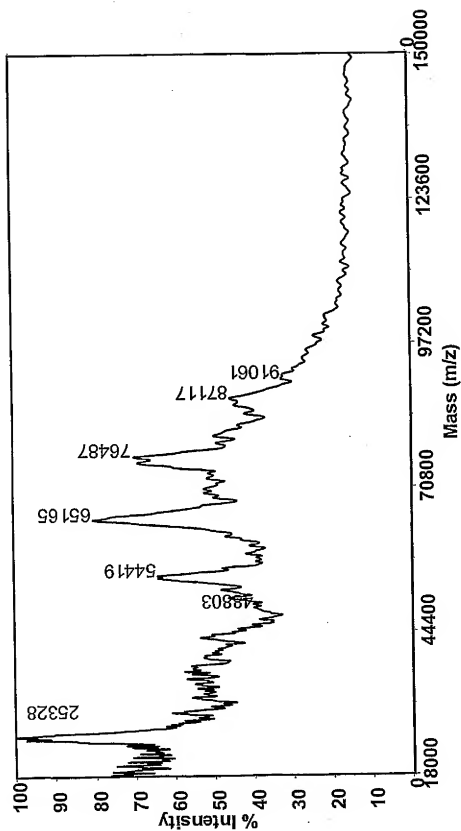


FIG. 119

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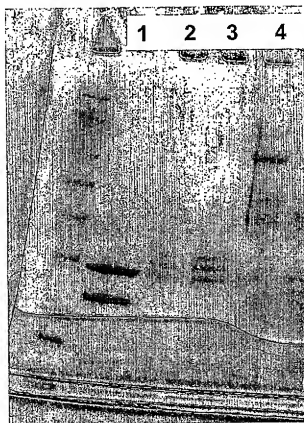


FIG. 120

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FIG. 121

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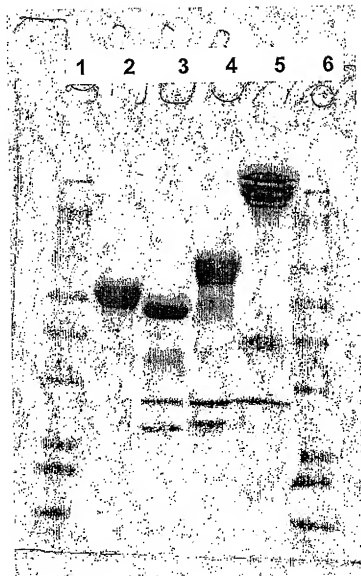


FIG. 122

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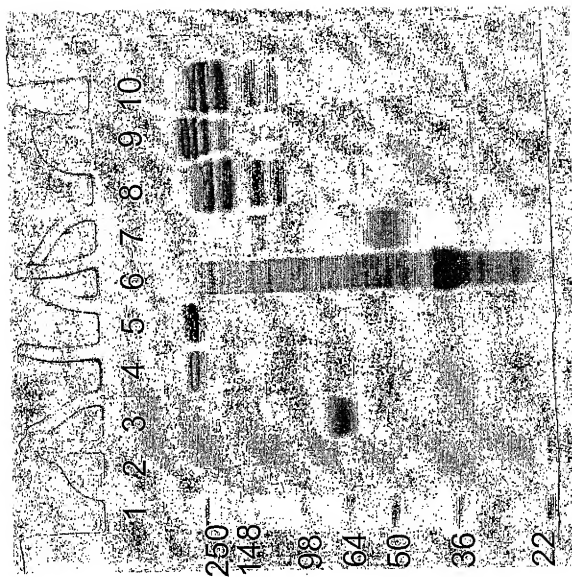


FIG. 123

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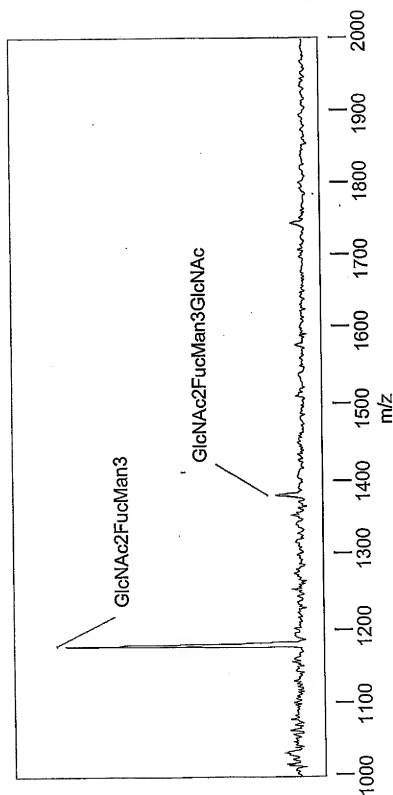


FIG. 124

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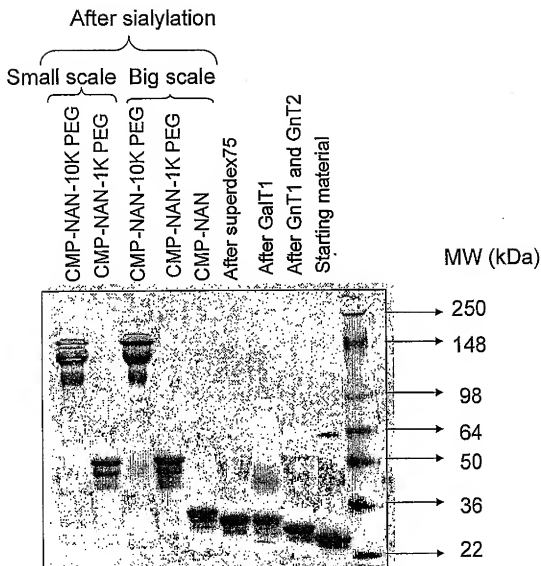


FIG. 125

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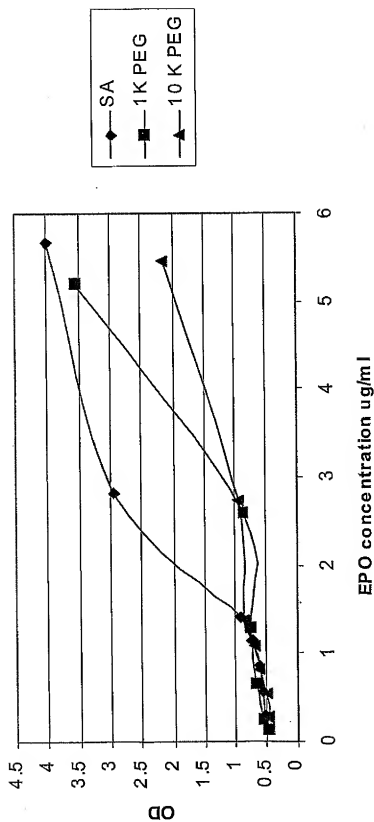


FIG. 126

SEQUENCE LISTING

<110> Neose Technologies, Inc.
 DeFrees, Shawn
 Zopf, David
 Bayer, Robert
 Bowe, Caryn
 Hakes, David
 Chen, Xi

<120> REMODELING AND GLYCOCONJUGATION OF PEPTIDES

<130> 040853-01-5050WO

<150> US 60/328,523

<151> 2001-10-10

<150> US 60/344,692

<151> 2001-10-19

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 20 25 30

Glu Lys Leu Cys Ala Thr Tyr Lys Leu Cys His Pro Glu Glu Leu Val
 35 40 45

Leu Leu Gly His Ser Leu Gly Ile Pro Trp Ala Pro Leu Ser Ser Cys
 50 55 60

Pro Ser Gln Ala Leu Gln Leu Ala Gly Cys Leu Ser Gln Leu His Ser
 65 70 75 80

Gly Leu Phe Leu Tyr Gln Gly Leu Leu Gln Ala Leu Glu Gly Ile Ser
 85 90 95

Pro Glu Leu Gly Pro Thr Leu Asp Thr Leu Gln Leu Asp Val Ala Asp
 100 105 110

Phe Ala Thr Thr Ile Trp Gln Gln Met Glu Glu Leu Gly Met Ala Pro
 115 120 125

Ala Leu Gln Pro Thr Gln Gly Ala Met Pro Ala Phe Ala Ser Ala Phe
 130 135 140

Gln Arg Arg Ala Gly Gly Val Leu Val Ala Ser His Leu Gln Ser Phe

145

150

155

160

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 20 25 30

Gly Ser Arg Arg Thr Leu Met Leu Leu Ala Gln Met Arg Arg Ile Ser
 35 40 45

Leu Phe Ser Cys Leu Lys Asp Arg His Asp Phe Gly Phe Pro Gln Glu
 50 55 60

Glu Phe Gly Asn Gln Phe Gln Lys Ala Glu Thr Ile Pro Val Leu His
 65 70 75 80

Glu Met Ile Gln Gln Ile Phe Asn Leu Phe Ser Thr Lys Asp Ser Ser
 85 90 95

Ala Ala Trp Asp Glu Thr Leu Leu Asp Lys Phe Tyr Thr Glu Leu Tyr
 100 105 110

Gln Gln Leu Asn Asp Leu Glu Ala Cys Val Ile Gln Gly Val Gly Val
 115 120 125

Thr Glu Thr Pro Leu Met Lys Glu Asp Ser Ile Leu Ala Val Arg Lys
 130 135 140

Tyr Phe Gln Arg Ile Thr Leu Tyr Leu Lys Glu Lys Lys Tyr Ser Pro
 145 150 155 160

Cys Ala Trp Glu Val Val Arg Ala Glu Ile Met Arg Ser Phe Ser Leu
 165 170 175

Ser Thr Asn Leu Gln Glu Ser Leu Arg Ser Lys Glu
 180 185

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<210> 6
 <211> 187
 <212> PRT
 <213> Homo sapiens

<400> 6

Met Thr Asn Lys Cys Leu Leu Gln Ile Ala Leu Leu Leu Cys Phe Ser
 1 5 10 15

Thr Thr Ala Leu Ser Met Ser Tyr Asn Leu Leu Gly Phe Leu Gln Arg
20 25 30

Ser Ser Asn Phe Gln Cys Gln Lys Leu Leu Trp Gln Leu Asn Gly Arg
35 40 45

Leu Glu Tyr Cys Leu Lys Asp Arg Met Asn Phe Asp Ile Pro Glu Glu
50 55 60

Ile Lys Gln Leu Gln Gln Phe Gln Lys Glu Asp Ala Ala Leu Thr Ile
65 70 75 80

Tyr Glu Met Leu Gln Asn Ile Phe Ala Ile Phe Arg Gln Asp Ser Ser
85 90 95

Ser Thr Gly Trp Asn Glu Thr Ile Val Glu Asn Leu Leu Ala Asn Val
100 105 110

Tyr His Gln Ile Asn His Leu Lys Thr Val Leu Glu Glu Lys Leu Glu
115 120 125

Lys Glu Asp Phe Thr Arg Gly Lys Leu Met Ser Ser Leu His Leu Lys
130 135 140

Arg Tyr Tyr Gly Arg Ile Leu His Tyr Leu Lys Ala Lys Glu Tyr Ser
145 150 155 160

His Cys Ala Trp Thr Ile Val Arg Val Glu Ile Leu Arg Asn Phe Tyr
165 170 175

Phe Ile Asn Arg Leu Thr Gly Tyr Leu Arg Asn
180 185

<210> 7

<211> 1332

<212> DNA

<213> Homo sapiens

<400> 7
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gcgttctctgg aggagctgcg gccgggctcc ctggagaggg agtgcaagga ggagcagtcg 180
tccttcgagg aggcccgga gatcttcaag gacgcggaga ggaogaagct gttctggatt 240

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acgcacaagg atgaccagct gatctgtgtg aacgagaacg gcggctgtga gcagtactgc 420
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gccccatttc cc

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<210> 8
 <211> 444
 <212> PRT
 <213> Homo sapiens

<400> 8

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Met Val Ser Gln Ala Leu Arg Leu Leu Cys Leu Leu Leu Gly Leu Gln
1          5          10          15

```

```

Gly Cys Leu Ala Ala Val Phe Val Thr Gln Glu Glu Ala His Gly Val
20          25          30

```

```

Leu His Arg Arg Arg Arg Ala Asn Ala Phe Leu Glu Glu Leu Arg Pro
35          40          45

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Gly Ser Leu Glu Arg Glu Cys Lys Glu Glu Gln Cys Ser Phe Glu Glu
50 55 60

Ala Arg Glu Ile Phe Lys Asp Ala Glu Arg Thr Lys Leu Phe Trp Ile
65 70 75 80

Ser Tyr Ser Asp Gly Asp Gln Cys Ala Ser Ser Pro Cys Gln Asn Gly
85 90 95

Gly Ser Cys Lys Asp Gln Leu Gln Ser Tyr Ile Cys Phe Cys Leu Pro
100 105 110

Ala Phe Glu Gly Arg Asn Cys Glu Thr His Lys Asp Asp Gln Leu Ile
115 120 125

Cys Val Asn Glu Asn Gly Gly Cys Glu Gln Tyr Cys Ser Asp His Thr
130 135 140

Gly Thr Lys Arg Ser Cys Arg Cys His Glu Gly Tyr Ser Leu Leu Ala
145 150 155 160

Asp Gly Val Ser Cys Thr Pro Thr Val Glu Tyr Pro Cys Gly Lys Ile
165 170 175

Pro Ile Leu Glu Lys Arg Asn Ala Ser Lys Pro Gln Gly Arg Ile Val
180 185 190

Gly Gly Lys Val Cys Pro Lys Gly Glu Cys Pro Trp Gln Val Leu Leu
195 200 205

Leu Val Asn Gly Ala Gln Leu Cys Gly Gly Thr Leu Ile Asn Thr Ile
210 215 220

Trp Val Val Ser Ala Ala His Cys Phe Asp Lys Ile Lys Asn Trp Arg
225 230 235 240

Asn Leu Ile Ala Val Leu Gly Glu His Asp Leu Ser Glu His Asp Gly
245 250 255

Asp Glu Gln Ser Arg Arg Val Ala Gln Val Ile Ile Pro Ser Thr Tyr
260 265 270

Val Pro Gly Thr Thr Asn His Asp Ile Ala Leu Leu Arg Leu His Gln
275 280 285

Pro Val Val Leu Thr Asp His Val Val Pro Leu Cys Leu Pro Glu Arg
290 295 300

Thr Phe Ser Glu Arg Thr Leu Ala Phe Val Arg Phe Ser Leu Val Ser
305 310 315 320

Gly Trp Gly Gln Leu Leu Asp Arg Gly Ala Thr Ala Leu Glu Leu Met
325 330 335

Val Leu Asn Val Pro Arg Leu Met Thr Gln Asp Cys Leu Gln Gln Ser
340 345 350

Arg Lys Val Gly Asp Ser Pro Asn Ile Thr Glu Tyr Met Phe Cys Ala
355 360 365

Gly Tyr Ser Asp Gly Ser Lys Asp Ser Cys Lys Gly Asp Ser Gly Gly
370 375 380

Pro His Ala Thr His Tyr Arg Gly Thr Trp Tyr Leu Thr Gly Ile Val
385 390 395 400

Ser Trp Gly Gln Gly Cys Ala Thr Val Gly His Phe Gly Val Tyr Thr
405 410 415

Arg Val Ser Gln Tyr Ile Glu Trp Leu Gln Lys Leu Met Arg Ser Glu
420 425 430

Pro Arg Pro Gly Val Leu Leu Arg Ala Pro Phe Pro
435 440

<210> 9
<211> 1437
<212> DNA
<213> Homo sapiens

<400> 9
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ggatatctac tcagtgctga atgtacagtt tttcttgatc atgaaaacgc caacaaaatt 120
ctgaatcgcc caaagaggta taattcaggt aaattggaag agtttggtca agggaacott 180

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gagagagaat gtatggaaga aaagtgtagt ttgagaac cagagaagt ttttgaaac 240
actgaaaaa caactgaatt ttggaagcag tatgttgatg gagatcagtg tgagtccaat 300
ccatgtttta atggcggcag ttgcaaggat gacattaatt cctatgaatg ttgggtgcc 360
tttggatttg aaggaaagaa ctgtgaatta gatgtaacat gtaacattaa gaatggcaga 420
tgcgagcagt tttgtaaaaa tagtgctgat aacaagggtg tttgctcctg tactgagggg 480
tatcgacttg cagaaaacca gaagtcctgt gaaccagcag tgcatttcc atgtggaaga 540
gtttctgttt cacaacttc taagctcacc cgtgctgagg ctgtttttcc tgatgtggac 600
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tttaatgact tcactcgggt tgttggtgga gaagatgcca aaccagggtca attccttgg 720
cagggtgttt tgaatggtaa agttgatgca ttctgtggag gctctatcgt taatgaaaaa 780
tggattgtaa ctgtgcccc ctgtgttgaa actggtgtta aaattacagt tgcgcagggt 840
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aaatattgaa tatataccaa ggtatccgg tatgtcaact ggattaagga aaaaacaaag 1380
ctcacttaat gaaagatgga ttccaagggt taattcattg gaattgaaaa ttaacag 1437

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<210> 10

<211> 462

<212> PRT

<213> Homo sapiens

<400> 10

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Met Gln Arg Val Asn Met Ile Met Ala Glu Ser Pro Ser Leu Ile Thr
1           5           10           15

```

```

Ile Cys Leu Leu Gly Tyr Leu Leu Ser Ala Glu Cys Thr Val Phe Leu
20           25           30

```

Asp His Glu Asn Ala Asn Lys Ile Leu Asn Arg Pro Lys Arg Tyr Asn
 35 40 45

Ser Gly Lys Leu Glu Glu Phe Val Gln Gly Asn Leu Glu Arg Glu Cys
 50 55 60

Met Glu Glu Lys Cys Ser Phe Glu Glu Pro Arg Glu Val Phe Glu Asn
 65 70 75 80

Thr Glu Lys Thr Thr Glu Phe Trp Lys Gln Tyr Val Asp Gly Asp Gln
 85 90 95

Cys Glu Ser Asn Pro Cys Leu Asn Gly Gly Ser Cys Lys Asp Asp Ile
 100 105 110

Asn Ser Tyr Glu Cys Trp Cys Pro Phe Gly Phe Glu Gly Lys Asn Cys
 115 120 125

Glu Leu Asp Val Thr Cys Asn Ile Lys Asn Gly Arg Cys Glu Gln Phe
 130 135 140

Cys Lys Asn Ser Ala Asp Asn Lys Val Val Cys Ser Cys Thr Glu Gly
 145 150 155 160

Tyr Arg Leu Ala Glu Asn Gln Lys Ser Cys Glu Pro Ala Val Pro Phe
 165 170 175

Pro Cys Gly Arg Val Ser Val Ser Gln Thr Ser Lys Leu Thr Arg Ala
 180 185 190

Glu Ala Val Phe Pro Asp Val Asp Tyr Val Asn Pro Thr Glu Ala Glu
 195 200 205

Thr Ile Leu Asp Asn Ile Thr Gln Gly Thr Gln Ser Phe Asn Asp Phe
 210 215 220

Thr Arg Val Val Gly Gly Glu Asp Ala Lys Pro Gly Gln Phe Pro Trp
 225 230 235 240

Gln Val Val Leu Asn Gly Lys Val Asp Ala Phe Cys Gly Gly Ser Ile
 245 250 255

Val Asn Glu Lys Trp Ile Val Thr Ala Ala His Cys Val Glu Thr Gly
 260 265 270

Val Lys Ile Thr Val Val Ala Gly Glu His Asn Ile Glu Glu Thr Glu
 275 280 285

His Thr Glu Gln Lys Arg Asn Val Ile Arg Ala Ile Ile Pro His His
 290 295 300

Asn Tyr Asn Ala Ala Ile Asn Lys Tyr Asn His Asp Ile Ala Leu Leu
 305 310 315 320

Glu Leu Asp Glu Pro Leu Val Leu Asn Ser Tyr Val Thr Pro Ile Cys
 325 330 335

Ile Ala Asp Lys Glu Tyr Thr Asn Ile Phe Leu Lys Phe Gly Ser Gly
 340 345 350

Tyr Val Ser Gly Trp Ala Arg Val Phe His Lys Gly Arg Ser Ala Leu
 355 360 365

Val Leu Gln Tyr Leu Arg Val Pro Leu Val Asp Arg Ala Thr Cys Leu
 370 375 380

Arg Ser Thr Lys Phe Thr Ile Tyr Asn Asn Met Phe Cys Ala Gly Phe
 385 390 395 400

His Glu Gly Gly Arg Asp Ser Cys Gln Gly Asp Ser Gly Gly Pro His
 405 410 415

Val Thr Glu Val Glu Gly Thr Ser Phe Leu Thr Gly Ile Ile Ser Trp
 420 425 430

Gly Glu Glu Cys Ala Met Lys Gly Lys Tyr Gly Ile Tyr Thr Lys Val
 435 440 445

Ser Arg Tyr Val Asn Trp Ile Lys Glu Lys Thr Lys Leu Thr
 450 455 460

<210> 11
 <211> 603
 <212> DNA
 <213> Homo sapiens

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<400> 11
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ttcttctccc agccgggtgc cccaatactt cagtgcattg gctgctgctt ctctagagca      180
tatccactc cactaaggtc caagaagaag atgttggtcc aaaagaacgt cacctcagag      240
tccacttgct gtgtagctaa atcatataac agggtcacag taatggggggg tttcaaagtg      300
gagaaccaca ogcggtgcc ctcagctact tgttattatc acaaatotta aatgttttac      360
caagtgtgtg ctgatgact gctgattttc tggaatggaa aattaagttg tttagtgttt      420
atggctttgt gagataaaac tctccttttc cttaccatac cactttgaca cgcttcaagg      480
atactagcga gctttactgc cttcctcctt atcctacagt acaatcagca gtctagttct      540
tttcatttgg aatgaataca gcattaagct tgttcactg caaataaagc cttttaaatc      600
atc                                                                           603

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<210> 12
<211> 116
<212> PRT
<213> Homo sapiens

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<400> 12

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Met Asp Tyr Tyr Arg Lys Tyr Ala Ala Ile Phe Leu Val Thr Leu Ser
1           5           10           15

```

```

Val Phe Leu His Val Leu His Ser Ala Pro Asp Val Gln Asp Cys Pro
          20           25           30

```

```

Glu Cys Thr Leu Gln Glu Asn Pro Phe Phe Ser Gln Pro Gly Ala Pro
          35           40           45

```

```

Ile Leu Gln Cys Met Gly Cys Cys Phe Ser Arg Ala Tyr Pro Thr Pro
          50           55           60

```

```

Leu Arg Ser Lys Lys Thr Met Leu Val Gln Lys Asn Val Thr Ser Glu
65           70           75           80

```

```

Ser Thr Cys Cys Val Ala Lys Ser Tyr Asn Arg Val Thr Val Met Gly
          85           90           95

```

```

Gly Phe Lys Val Glu Asn His Thr Ala Cys His Cys Ser Thr Cys Tyr
          100          105          110

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Tyr His Lys Ser
115

<210> 13
<211> 390
<212> DNA
<213> Homo sapiens

<400> 13
atgaagacac tccagttttt cttccttttc tgttgctgga aagcaatctg ctgcaatagc 60
tgtgagctga ccaacatcac cattgcaata gagaagaag aatgtcgttt ctgcataagc 120
atcaacacca cttggtgtgc tggctactgc tacaccaggg atctggtgta taaggacca 180
gccaggccca aaatccagaa aacatgtacc ttcaaggaac tggatatga aacagtgaga 240
gtgcccggt gtgctcacca tgcagattcc ttgtatacat acccagtggc caccagtgt 300
cactgtggca agtgtgacag cgacagcact gattgtactg tgcgaggcct ggggccacgc 360
tactgtctct ttggtgaaat gaaagaataa 390

<210> 14
<211> 129
<212> PRT
<213> Homo sapiens

<400> 14

Met Lys Thr Leu Gln Phe Phe Phe Leu Phe Cys Cys Trp Lys Ala Ile
1 5 10 15

Cys Cys Asn Ser Cys Glu Leu Thr Asn Ile Thr Ile Ala Ile Glu Lys
20 25 30

Glu Glu Cys Arg Phe Cys Ile Ser Ile Asn Thr Thr Trp Cys Ala Gly
35 40 45

Tyr Cys Tyr Thr Arg Asp Leu Val Tyr Lys Asp Pro Ala Arg Pro Lys
50 55 60

Ile Gln Lys Thr Cys Thr Phe Lys Glu Leu Val Tyr Glu Thr Val Arg
65 70 75 80

Val Pro Gly Cys Ala His His Ala Asp Ser Leu Tyr Thr Tyr Pro Val
85 90 95

Ala Thr Gln Cys His Cys Gly Lys Cys Asp Ser Asp Ser Thr Asp Cys
 100 105 110

Thr Val Arg Gly Leu Gly Pro Ser Tyr Cys Ser Phe Gly Glu Met Lys
 115 120 125

Glu

<210> 15
 <211> 1342
 <212> DNA
 <213> Homo sapiens

<400> 15
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 ccgcctctc ctccaggccc gtggggctgg cctgcaccc cggagcttc cgggatgagg 120
 gccccgggtg tggtcaccgc gcgcgcccca ggctgctgag ggaccccgcc caggcgcgga 180
 gatgggggtg cacgaatgtc ctgcttggtg gtgcttctc ctgtccctgc tgtgctccc 240
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 gaggtagctc ttggaggcca aggaggccga gaatatcac acgggctgtg ctgaacactg 360
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 gatggaggtc gggcagcagg ccgtagaagt ctggcagggc ctggccctgc tgtcggaagc 480
 tgtctgcgg ggccaggccc tgttggtcaa ctctccag ccgtgggagc cctgcagct 540
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 agccagaag gaagccatct cccctccaga tgcggcctca gtgctccac tccgaacaat 660
 cactgtgac actttccgca aactcttcgc agtctactcc aatttctcgc ggggaagct 720
 gaagctgtac acaggggagg cctgcaggac aggggacaga tgaccaggtg tgtccacctg 780
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 ggacagagcc atgctgggaa gacgcctgag ctactcggc accctgcaaa atttgatgcc 1080
 aggacacgct ttggaggcga tttaacctgt ttgcaccta ccactcagga caggatgacc 1140

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tgggagaactt aggtgggcaag ctgtgacttc tccaggtctc acgggcatgg gcactccctt 1200
ggtgggcaaga gccccttga caccggggtg gtgggaacca tgaagacagg atgggggctg 1260
gcctctgggt ctcctgggt ccaagttttg tgtattcttc aacctcattg acaagaactg 1320
aaaccaccaa aaaaaaaaaa aa 1342

```

```

<210> 16
<211> 193
<212> PRT
<213> Homo sapiens

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```

<400> 16

```

```

Met Gly Val His Glu Cys Pro Ala Trp Leu Trp Leu Leu Leu Ser Leu
1           5           10           15

```

```

Leu Ser Leu Pro Leu Gly Leu Pro Val Leu Gly Ala Pro Pro Arg Leu
          20           25           30

```

```

Ile Cys Asp Ser Arg Val Leu Glu Arg Tyr Leu Leu Glu Ala Lys Glu
          35           40           45

```

```

Ala Glu Asn Ile Thr Thr Gly Cys Ala Glu His Cys Ser Leu Asn Glu
          50           55           60

```

```

Asn Ile Thr Val Pro Asp Thr Lys Val Asn Phe Tyr Ala Trp Lys Arg
65           70           75           80

```

```

Met Glu Val Gly Gln Gln Ala Val Glu Val Trp Gln Gly Leu Ala Leu
          85           90           95

```

```

Leu Ser Glu Ala Val Leu Arg Gly Gln Ala Leu Leu Val Asn Ser Ser
          100          105          110

```

```

Gln Pro Trp Glu Pro Leu Gln Leu His Val Asp Lys Ala Val Ser Gly
          115          120          125

```

```

Leu Arg Ser Leu Thr Thr Leu Leu Arg Ala Leu Arg Ala Gln Lys Glu
          130          135          140

```

```

Ala Ile Ser Pro Pro Asp Ala Ala Ser Ala Ala Pro Leu Arg Thr Ile
          145          150          155          160

```

```

Thr Ala Asp Thr Phe Arg Lys Leu Phe Arg Val Tyr Ser Asn Phe Leu

```

165

170

175

Arg Gly Lys Leu Lys Leu Tyr Thr Gly Glu Ala Cys Arg Thr Gly Asp
 180 185 190

Arg

<210> 17
 <211> 435
 <212> DNA
 <213> Homo sapiens

<400> 17
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 cgctcgccca gccccagcac gcagccctgg gagcatgtga atgccatcca ggaggcccg 120
 cgtctcctga acctgagtag agacactgct gctgagatga atgaaacagt agaagtcac 180
 tcagaaatgt ttgacctcca ggagccgacc tgcctacaga ccogcctgga gctgtacaag 240
 cagggcctgc ggggcagcct caccaagctc aagggccctc tgaccatgat gccagccac 300
 tacaagcagc actgccctcc aaccccgaa acttctctgt caaccagat tatcaccttt 360
 gaaagtcca aagagaacct gaaggacttt ctgcttctga tcccccttga ctgctgggag 420
 ccagtccagg agtga 435

<210> 18
 <211> 144
 <212> PRT
 <213> Homo sapiens

<400> 18

Met Trp Leu Gln Ser Leu Leu Leu Gly Thr Val Ala Cys Ser Ile
 1 5 10 15

Ser Ala Pro Ala Arg Ser Pro Ser Pro Ser Thr Gln Pro Trp Glu His
 20 25 30

Val Asn Ala Ile Gln Glu Ala Arg Arg Leu Leu Asn Leu Ser Arg Asp
 35 40 45

Thr Ala Ala Glu Met Asn Glu Thr Val Glu Val Ile Ser Glu Met Phe
 50 55 60

Asp Leu Gln Glu Pro Thr Cys Leu Gln Thr Arg Leu Glu Leu Tyr Lys
 65 70 75 80

Gln Gly Leu Arg Gly Ser Leu Thr Lys Leu Lys Gly Pro Leu Thr Met
 85 90 95

Met Ala Ser His Tyr Lys Gln His Cys Pro Pro Thr Pro Glu Thr Ser
 100 105 110

Cys Ala Thr Gln Ile Ile Thr Phe Glu Ser Phe Lys Glu Asn Leu Lys
 115 120 125

Asp Phe Leu Leu Val Ile Pro Phe Asp Cys Trp Glu Pro Val Gln Glu
 130 135 140

<210> 19
 <211> 501
 <212> DNA
 <213> Homo sapiens

<400> 19
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 ggtcattcag atgtagcgga taatggaact cttttcttag gcattttgaa gaattggaaa 180
 gaggagagtg acagaaaaat aatgcagagc caaattgtct cttttactt caaacttttt 240
 aaaaacttta aagatgacca gagcatccaa aagagtgtgg agaccatcaa ggaagacatg 300
 aatgtcaagt ttttcaatag caacaaaaag aaacgagatg acttcgaaaa gctgactaat 360
 tattcggttaa ctgacttgaa tgccaacgc aaagcaatac atgaactcat ccaagtgatg 420
 gctgaactgt cgccagcagc taaaacaggg aagcgaaaaa ggagtcagat gctgtttcga 480
 ggtcgaagag catccagta a 501

<210> 20
 <211> 166
 <212> PRT
 <213> Homo sapiens

<400> 20

Met Lys Tyr Thr Ser Tyr Ile Leu Ala Phe Gln Leu Cys Ile Val Leu
 1 5 10 15

Gly Ser Leu Gly Cys Tyr Cys Gln Asp Pro Tyr Val Lys Glu Ala Glu

20

25

30

Asn Leu Lys Lys Tyr Phe Asn Ala Gly His Ser Asp Val Ala Asp Asn
 35 40 45

Gly Thr Leu Phe Leu Gly Ile Leu Lys Asn Trp Lys Glu Glu Ser Asp
 50 55 60

Arg Lys Ile Met Gln Ser Gln Ile Val Ser Phe Tyr Phe Lys Leu Phe
 65 70 75 80

Lys Asn Phe Lys Asp Asp Gln Ser Ile Gln Lys Ser Val Glu Thr Ile
 85 90 95

Lys Glu Asp Met Asn Val Lys Phe Phe Asn Ser Asn Lys Lys Lys Arg
 100 105 110

Asp Asp Phe Glu Lys Leu Thr Asn Tyr Ser Val Thr Asp Leu Asn Val
 115 120 125

Gln Arg Lys Ala Ile His Glu Leu Ile Gln Val Met Ala Glu Leu Ser
 130 135 140

Pro Ala Ala Lys Thr Gly Lys Arg Lys Arg Ser Gln Met Leu Phe Arg
 145 150 155 160

Gly Arg Arg Ala Ser Gln
 165

<210> 21

<211> 1352

<212> DNA

<213> Homo sapiens

<400> 21

ctgggacagt gaatcgacaa tgccgtcttc tgtctcgtgg ggcatactcc tgcctggcagg 60
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 gacagataca tcccacatg atcaggatca cccaaccttc aacaagatca cccccaacct 180
 ggctgagttc gccttcagcc tataccgcc gctggcacac cagtccaaca gcaccaatat 240
 cttctctctc ccagtgagca tcgtacagc ctttgcaatg ctctccttgg ggaccaaggc 300
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tcagatccat gaaggcttcc aggaactcct ccgtaccctc aaccagccag acagccagct 420
 ccagctgacc accggcaatg gcctgttccct cagcgagggc ctgaagctag tggataagtt 480
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 cgaagaggcc aagaaacaga tcaacgatta cgtggagaag ggtactcaag ggaaaattgt 600
 ggatttggtc aaggagcttg acagagacac agtttttgct ctgggtgaatt acatcttctt 660
 taaaggcaaa tgggagagac cctttgaagt caaggacacc gaggaagagg acttccacgt 720
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 ccctggatga cattaaagaa ggggtgagct gg 1352

<210> 22
 <211> 418
 <212> PRT
 <213> Homo sapiens

<400> 22

Met Pro Ser Ser Val Ser Trp Gly Ile Leu Leu Leu Ala Gly Leu Cys
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Cys Leu Val Pro Val Ser Leu Ala Glu Asp Pro Gln Gly Asp Ala Ala
 20 25 30

Gln Lys Thr Asp Thr Ser His His Asp Gln Asp His Pro Thr Phe Asn
 35 40 45

Lys Ile Thr Pro Asn Leu Ala Glu Phe Ala Phe Ser Leu Tyr Arg Gln
 50 55 60

Leu Ala His Gln Ser Asn Ser Thr Asn Ile Phe Phe Ser Pro Val Ser
 65 70 75 80

Ile Ala Thr Ala Phe Ala Met Leu Ser Leu Gly Thr Lys Ala Asp Thr
 85 90 95

His Asp Glu Ile Leu Glu Gly Leu Asn Phe Asn Leu Thr Glu Ile Pro
 100 105 110

Glu Ala Gln Ile His Glu Gly Phe Gln Glu Leu Leu Arg Thr Leu Asn
 115 120 125

Gln Pro Asp Ser Gln Leu Gln Leu Thr Thr Gly Asn Gly Leu Phe Leu
 130 135 140

Ser Glu Gly Leu Lys Leu Val Asp Lys Phe Leu Glu Asp Val Lys Lys
 145 150 155 160

Leu Tyr His Ser Glu Ala Phe Thr Val Asn Phe Gly Asp Thr Glu Glu
 165 170 175

Ala Lys Lys Gln Ile Asn Asp Tyr Val Glu Lys Gly Thr Gln Gly Lys
 180 185 190

Ile Val Asp Leu Val Lys Glu Leu Asp Arg Asp Thr Val Phe Ala Leu
 195 200 205

Val Asn Tyr Ile Phe Phe Lys Gly Lys Trp Glu Arg Pro Phe Glu Val
 210 215 220

Lys Asp Thr Glu Glu Glu Asp Phe His Val Asp Gln Val Thr Thr Val
 225 230 235 240

Lys Val Pro Met Met Lys Arg Leu Gly Met Phe Asn Ile Gln His Cys
 245 250 255

Lys Lys Leu Ser Ser Trp Val Leu Leu Met Lys Tyr Leu Gly Asn Ala
 260 265 270

Thr Ala Ile Phe Phe Leu Pro Asp Glu Gly Lys Leu Gln His Leu Glu
 275 280 285

Asn Glu Leu Thr His Asp Ile Ile Thr Lys Phe Leu Glu Asn Glu Asp
 290 295 300

Arg Arg Ser Ala Ser Leu His Leu Pro Lys Leu Ser Ile Thr Gly Thr
 305 310 315 320

Tyr Asp Leu Lys Ser Val Leu Gly Gln Leu Gly Ile Thr Lys Val Phe
 325 330 335

Ser Asn Gly Ala Asp Leu Ser Gly Val Thr Glu Glu Ala Pro Leu Lys
 340 345 350

Leu Ser Lys Ala Val His Lys Ala Val Leu Thr Ile Asp Glu Lys Gly
 355 360 365

Thr Glu Ala Ala Gly Ala Met Phe Leu Glu Ala Ile Pro Met Ser Ile
 370 375 380

Pro Pro Glu Val Lys Phe Asn Lys Pro Phe Val Phe Leu Met Ile Glu
 385 390 395 400

Gln Asn Thr Lys Ser Pro Leu Phe Met Gly Lys Val Val Asn Pro Thr
 405 410 415

Gln Lys

<210> 23
 <211> 2004
 <212> DNA
 <213> Homo sapiens

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<210> 24
 <211> 536
 <212> PRT

<213> Homo sapiens

<400> 24

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Arg Val Ser Ile Met Ala Gly Ser Leu Thr Gly Leu Leu Leu Gln
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Ala Val Ser Trp Ala Ser Gly Ala Arg Pro Cys Ile Pro Lys Ser Phe
 35 40 45

Gly Tyr Ser Ser Val Val Cys Val Cys Asn Ala Thr Tyr Cys Asp Ser
 50 55 60

Phe Asp Pro Pro Thr Phe Pro Ala Leu Gly Thr Phe Ser Arg Tyr Glu
 65 70 75 80

Ser Thr Arg Ser Gly Arg Arg Met Glu Leu Ser Met Gly Pro Ile Gln
 85 90 95

Ala Asn His Thr Gly Thr Gly Leu Leu Leu Thr Leu Gln Pro Glu Gln
 100 105 110

Lys Phe Gln Lys Val Lys Gly Phe Gly Gly Ala Met Thr Asp Ala Ala
 115 120 125

Ala Leu Asn Ile Leu Ala Leu Ser Pro Pro Ala Gln Asn Leu Leu Leu
 130 135 140

Lys Ser Tyr Phe Ser Glu Glu Gly Ile Gly Tyr Asn Ile Ile Arg Val
 145 150 155 160

Pro Met Ala Ser Cys Asp Phe Ser Ile Arg Thr Tyr Thr Tyr Ala Asp
 165 170 175

Thr Pro Asp Asp Phe Gln Leu His Asn Phe Ser Leu Pro Glu Glu Asp
 180 185 190

Thr Lys Leu Lys Ile Pro Leu Ile His Arg Ala Leu Gln Leu Ala Gln
 195 200 205

Arg Pro Val Ser Leu Leu Ala Ser Pro Trp Thr Ser Pro Thr Trp Leu

210	215	220
Lys Thr Asn Gly Ala Val Asn Gly Lys Gly Ser Leu Lys Gly Gln Pro 225 230 235 240		
Gly Asp Ile Tyr His Gln Thr Trp Ala Arg Tyr Phe Val Lys Phe Leu 245 250 255		
Asp Ala Tyr Ala Glu His Lys Leu Gln Phe Trp Ala Val Thr Ala Glu 260 265 270		
Asn Glu Pro Ser Ala Gly Leu Leu Ser Gly Tyr Pro Phe Gln Cys Leu 275 280 285		
Gly Phe Thr Pro Glu His Gln Arg Asp Phe Ile Ala Arg Asp Leu Gly 290 295 300		
Pro Thr Leu Ala Asn Ser Thr His His Asn Val Arg Leu Leu Met Leu 305 310 315 320		
Asp Asp Gln Arg Leu Leu Leu Pro His Trp Ala Lys Val Val Leu Thr 325 330 335		
Asp Pro Glu Ala Ala Lys Tyr Val His Gly Ile Ala Val His Tyr Tyr 340 345 350		
Leu Asp Phe Leu Ala Pro Ala Lys Ala Thr Leu Gly Glu Thr His Arg 355 360 365		
Leu Phe Pro Asn Thr Met Leu Phe Ala Ser Glu Ala Cys Val Gly Ser 370 375 380		
Lys Phe Trp Glu Gln Ser Val Arg Leu Gly Ser Trp Asp Arg Gly Met 385 390 395 400		
Gln Tyr Ser His Ser Ile Ile Thr Asn Leu Leu Tyr His Val Val Gly 405 410 415		
Trp Thr Asp Trp Asn Leu Ala Leu Asn Pro Glu Gly Gly Pro Asn Trp 420 425 430		
Val Arg Asn Phe Val Asp Ser Pro Ile Ile Val Asp Ile Thr Lys Asp 435 440 445		

Thr Phe Tyr Lys Gln Pro Met Phe Tyr His Leu Gly His Phe Ser Lys
 450 455 460

Phe Ile Pro Glu Gly Ser Gln Arg Val Gly Leu Val Ala Ser Gln Lys
 465 470 475 480

Asn Asp Leu Asp Ala Val Ala Leu Met His Pro Asp Gly Ser Ala Val
 485 490 495

Val Val Val Leu Asn Arg Ser Ser Lys Asp Val Pro Leu Thr Ile Lys
 500 505 510

Asp Pro Ala Val Gly Phe Leu Glu Thr Ile Ser Pro Gly Tyr Ser Ile
 515 520 525

His Thr Tyr Leu Trp His Arg Gln
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<210> 25
 <211> 1726
 <212> DNA
 <213> Homo sapiens

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 gtgcctgtca aaagttgcag cgagccaagg tgtttcaacg ggggcacctg ccagcaggcc 300
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 tcagcctacc gtggcacgca cagcctcacc ggtcgggtg cctcctgcct cccgtggaat 720
 tccatgatcc tgataggcaa ggtttacaca gcacagaacc ccagtgcaca ggcactgggc 780

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gatgtccogg gtgtgtacac caagggtacc aactacctag actggattcg tgacaacatg     1680
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<210> 26

<211> 562

<212> PRT

<213> Homo sapiens

<400> 26

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Met Asp Ala Met Lys Arg Gly Leu Cys Cys Val Leu Leu Leu Cys Gly
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Ala Val Phe Val Ser Pro Ser Gln Glu Ile His Ala Arg Phe Arg Arg
20           25           30

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Gly Ala Arg Ser Tyr Gln Val Ile Cys Arg Asp Glu Lys Thr Gln Met
35           40           45

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Ile Tyr Gln Gln His Gln Ser Trp Leu Arg Pro Val Leu Arg Ser Asn
50           55           60

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Arg Val Glu Tyr Cys Trp Cys Asn Ser Gly Arg Ala Gln Cys His Ser
 65 70 75 80

Val Pro Val Lys Ser Cys Ser Glu Pro Arg Cys Phe Asn Gly Gly Thr
 85 90 95

Cys Gln Gln Ala Leu Tyr Phe Ser Asp Phe Val Cys Gln Cys Pro Glu
 100 105 110

Gly Phe Ala Gly Lys Cys Cys Glu Ile Asp Thr Arg Ala Thr Cys Tyr
 115 120 125

Glu Asp Gln Gly Ile Ser Tyr Arg Gly Thr Trp Ser Thr Ala Glu Ser
 130 135 140

Gly Ala Glu Cys Thr Asn Trp Asn Ser Ser Ala Leu Ala Gln Lys Pro
 145 150 155 160

Tyr Ser Gly Arg Arg Pro Asp Ala Ile Arg Leu Gly Leu Gly Asn His
 165 170 175

Asn Tyr Cys Arg Asn Pro Asp Arg Asp Ser Lys Pro Trp Cys Tyr Val
 180 185 190

Phe Lys Ala Gly Lys Tyr Ser Ser Glu Phe Cys Ser Thr Pro Ala Cys
 195 200 205

Ser Glu Gly Asn Ser Asp Cys Tyr Phe Gly Asn Gly Ser Ala Tyr Arg
 210 215 220

Gly Thr His Ser Leu Thr Glu Ser Gly Ala Ser Cys Leu Pro Trp Asn
 225 230 235 240

Ser Met Ile Leu Ile Gly Lys Val Tyr Thr Ala Gln Asn Pro Ser Ala
 245 250 255

Gln Ala Leu Gly Leu Gly Lys His Asn Tyr Cys Arg Asn Pro Asp Gly
 260 265 270

Asp Ala Lys Pro Trp Cys His Val Leu Lys Asn Arg Arg Leu Thr Trp
 275 280 285

Glu Tyr Cys Asp Val Pro Ser Cys Ser Thr Cys Gly Leu Arg Gln Tyr

290

295

300

Ser Gln Pro Gln Phe Arg Ile Lys Gly Gly Leu Phe Ala Asp Ile Ala
305 310 315 320

Ser His Pro Trp Gln Ala Ala Ile Phe Ala Lys His Arg Arg Ser Pro
325 330 335

Gly Glu Arg Phe Leu Cys Gly Gly Ile Leu Ile Ser Ser Cys Trp Ile
340 345 350

Leu Ser Ala Ala His Cys Phe Gln Glu Arg Phe Pro Pro His His Leu
355 360 365

Thr Val Ile Leu Gly Arg Thr Tyr Arg Val Val Pro Gly Glu Glu Glu
370 375 380

Gln Lys Phe Glu Val Glu Lys Tyr Ile Val His Lys Glu Phe Asp Asp
385 390 395 400

Asp Thr Tyr Asp Asn Asp Ile Ala Leu Leu Gln Leu Lys Ser Asp Ser
405 410 415

Ser Arg Cys Ala Gln Glu Ser Ser Val Val Arg Thr Val Cys Leu Pro
420 425 430

Pro Ala Asp Leu Gln Leu Pro Asp Trp Thr Glu Cys Glu Leu Ser Gly
435 440 445

Tyr Gly Lys His Glu Ala Leu Ser Pro Phe Tyr Ser Glu Arg Leu Lys
450 455 460

Glu Ala His Val Arg Leu Tyr Pro Ser Ser Arg Cys Thr Ser Gln His
465 470 475 480

Leu Leu Asn Arg Thr Val Thr Asp Asn Met Leu Cys Ala Gly Asp Thr
485 490 495

Arg Ser Gly Gly Pro Gln Ala Asn Leu His Asp Ala Cys Gln Gly Asp
500 505 510

Ser Gly Gly Pro Leu Val Cys Leu Asn Asp Gly Arg Met Thr Leu Val
515 520 525

Gly Ile Ile Ser Trp Gly Leu Gly Cys Gly Gln Lys Asp Val Pro Gly
 530 535 540

Val Tyr Thr Lys Val Thr Asn Tyr Leu Asp Trp Ile Arg Asp Asn Met
 545 550 555 560

Arg Pro

<210> 27
 <211> 825
 <212> DNA
 <213> Homo sapiens

<400> 27
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 tttataaat ttgataata taaaaaaaaa aacaaaaaaa aaaa 825

<210> 28
 <211> 156
 <212> PRT
 <213> Homo sapiens

<400> 28

Met Tyr Arg Met Gln Leu Leu Ser Cys Ile Ala Leu Ile Leu Ala Leu

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Thr Gln Leu Gln Leu Glu His Leu Leu Asp Leu Gln Met Ile Leu	35	40	45
Asn Gly Ile Asn Asn Tyr Lys Asn Pro Lys Leu Thr Arg Met Leu Thr	50	55	60
Phe Lys Phe Tyr Met Pro Lys Lys Ala Thr Glu Leu Lys Gln Leu Gln	65	70	75
Cys Leu Glu Glu Glu Leu Lys Pro Leu Glu Glu Val Leu Asn Leu Ala	85	90	95
Gln Ser Lys Asn Phe His Leu Arg Pro Arg Asp Leu Ile Ser Asn Ile	100	105	110
Asn Val Ile Val Leu Glu Leu Lys Gly Ser Glu Thr Thr Phe Met Cys	115	120	125
Glu Tyr Ala Asp Glu Thr Ala Thr Ile Val Glu Phe Leu Asn Arg Trp	130	135	140
Ile Thr Phe Cys Gln Ser Ile Ile Ser Thr Leu Thr	145	150	155

<210> 29

<211> 7931

<212> DNA

<213> Homo sapiens

<400> 29

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Trp Asp Tyr Met Gln Ser Asp Leu Gly Glu Leu Pro Val Asp Ala Arg
          35           40           45

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Phe Pro Pro Arg Val Pro Lys Ser Phe Pro Phe Asn Thr Ser Val Val
50           55           60

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Tyr Lys Lys Thr Leu Phe Val Glu Phe Thr Asp His Leu Phe Asn Ile
65           70           75           80

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Ala Lys Pro Arg Pro Pro Trp Met Gly Leu Leu Gly Pro Thr Ile Gln
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His Pro Val Ser Leu His Ala Val Gly Val Ser Tyr Trp Lys Ala Ser
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Glu Gly Ala Glu Tyr Asp Asp Gln Thr Ser Gln Arg Glu Lys Glu Asp
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Asp Lys Val Phe Pro Gly Gly Ser His Thr Tyr Val Trp Gln Val Leu
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Lys Glu Asn Gly Pro Met Ala Ser Asp Pro Leu Cys Leu Thr Tyr Ser
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Tyr Leu Ser His Val Asp Leu Val Lys Asp Leu Asn Ser Gly Leu Ile
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Gly Ala Leu Leu Val Cys Arg Glu Gly Ser Leu Ala Lys Glu Lys Thr
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Gln Thr Leu His Lys Phe Ile Leu Leu Phe Ala Val Phe Asp Glu Gly
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Val Asn Arg Ser Leu Pro Gly Leu Ile Gly Cys His Arg Lys Ser Val
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Tyr Trp His Val Ile Gly Met Gly Thr Thr Pro Glu Val His Ser Ile
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Phe Leu Glu Gly His Thr Phe Leu Val Arg Asn His Arg Gln Ala Ser
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His Gly Ile Thr Asp Val Arg Pro Leu Tyr Ser Arg Arg Leu Pro Lys
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Gly Val Lys His Leu Lys Asp Phe Pro Ile Leu Pro Gly Glu Ile Phe
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Pro Arg Cys Leu Thr Arg Tyr Tyr Ser Ser Phe Val Asn Met Glu Arg

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Ser Val Asp Gln Arg Gly Asn Gln Ile Met Ser Asp Lys Arg Asn Val	580	585	590
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Pro Glu Phe Gln Ala Ser Asn Ile Met His Ser Ile Asn Gly Tyr Val	625	630	635
Phe Asp Ser Leu Gln Leu Ser Val Cys Leu His Glu Val Ala Tyr Trp	645	650	655
Tyr Ile Leu Ser Ile Gly Ala Gln Thr Asp Phe Leu Ser Val Phe Phe	660	665	670
Ser Gly Tyr Thr Phe Lys His Lys Met Val Tyr Glu Asp Thr Leu Thr	675	680	685
Leu Phe Pro Phe Ser Gly Glu Thr Val Phe Met Ser Met Glu Asn Pro	690	695	700
Gly Leu Trp Ile Leu Gly Cys His Asn Ser Asp Phe Arg Asn Arg Gly	705	710	715
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Ser Thr Arg Gln Lys Gln Phe Asn Ala Thr Thr Ile Pro Glu Asn Asp	770	775	780

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Glu Thr Phe Ser Asp Asp Pro Ser Pro Gly Ala Ile Asp Ser Asn Asn
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Ser Leu Ser Glu Met Thr His Phe Arg Pro Gln Leu His His Ser Gly
850 855 860

Asp Met Val Phe Thr Pro Glu Ser Gly Leu Gln Leu Arg Leu Asn Glu
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Lys Leu Gly Thr Thr Ala Ala Thr Glu Leu Lys Lys Leu Asp Phe Lys
885 890 895

Val Ser Ser Thr Ser Asn Asn Leu Ile Ser Thr Ile Pro Ser Asp Asn
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Leu Ala Ala Gly Thr Asp Asn Thr Ser Ser Leu Gly Pro Pro Ser Met
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Pro Val His Tyr Asp Ser Gln Leu Asp Thr Thr Leu Phe Gly Lys Lys
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Asn Asn Asp Ser Lys Leu Leu Glu Ser Gly Leu Met Asn Ser Gln Glu
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Ser Ser Trp Gly Lys Asn Val Ser Ser Thr Glu Ser Gly Arg Leu Phe
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Lys Gly Lys Arg Ala His Gly Pro Ala Leu Leu Thr Lys Asp Asn Ala
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Asn Asn Ser Ala Thr Asn Arg Lys Thr His Ile Asp Gly Pro Ser
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 gtcacctgca tcgtgaacgt ctgtagcagc tctgaccaca gtcacagtgc ctctcccaa 1200
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 ctggggagca ccgaagagaa gcccctgccc ctggagtgcc ctgatgctgg gatgaagccc 1380
 agttaaccag gccggtgtgg gctgtgtcgt agccaagtg ggctgagccc tggcaggatg 1440
 accctgcgaa ggggccctgg tcctccagg c 1471

<210> 32
 <211> 461
 <212> FRT
 <213> Homo sapiens

<400> 32

Met Ala Pro Val Ala Val Trp Ala Ala Leu Ala Val Gly Leu Glu Leu
 1 5 10 15

Trp Ala Ala Ala His Ala Leu Pro Ala Gln Val Ala Phe Thr Pro Tyr
 20 25 30

Ala Pro Glu Pro Gly Ser Thr Cys Arg Leu Arg Glu Tyr Tyr Asp Gln
 35 40 45

Thr Ala Gln Met Cys Cys Ser Lys Cys Ser Pro Gly Gln His Ala Lys
 50 55 60

Val Phe Cys Thr Lys Thr Ser Asp Thr Val Cys Asp Ser Cys Glu Asp
 65 70 75 80

Ser Thr Tyr Thr Gln Leu Trp Asn Trp Val Pro Glu Cys Leu Ser Cys
 85 90 95

Gly Ser Arg Cys Ser Ser Asp Gln Val Glu Thr Gln Ala Cys Thr Arg
 100 105 110

Glu Gln Asn Arg Ile Cys Thr Cys Arg Pro Gly Trp Tyr Cys Ala Leu
 115 120 125

Ser Lys Gln Glu Gly Cys Arg Leu Cys Ala Pro Leu Arg Lys Cys Arg
 130 135 140

Pro Gly Phe Gly Val Ala Arg Pro Gly Thr Glu Thr Ser Asp Val Val
 145 150 155 160

Cys Lys Pro Cys Ala Pro Gly Thr Phe Ser Asn Thr Thr Ser Ser Thr
 165 170 175

Asp Ile Cys Arg Pro His Gln Ile Cys Asn Val Val Ala Ile Pro Gly
 180 185 190

Asn Ala Ser Met Asp Ala Val Cys Thr Ser Thr Ser Pro Thr Arg Ser
 195 200 205

Met Ala Pro Gly Ala Val His Leu Pro Gln Pro Val Ser Thr Arg Ser
 210 215 220

Gln His Thr Gln Pro Thr Pro Glu Pro Ser Thr Ala Pro Ser Thr Ser
 225 230 235 240

Phe Leu Leu Pro Met Gly Pro Ser Pro Pro Ala Glu Gly Ser Thr Gly
 245 250 255

Asp Phe Ala Leu Pro Val Gly Leu Ile Val Gly Val Thr Ala Leu Gly
 260 265 270

Leu Leu Ile Ile Gly Val Val Asn Cys Val Ile Met Thr Gln Val Lys
 275 280 285

Lys Lys Pro Leu Cys Leu Gln Arg Glu Ala Lys Val Pro His Leu Pro
 290 295 300

Ala Asp Lys Ala Arg Gly Thr Gln Gly Pro Glu Gln Gln His Leu Leu
 305 310 315 320

Ile Thr Ala Pro Ser Ser Ser Ser Ser Ser Leu Glu Ser Ser Ala Ser
 325 330 335

Ala Leu Asp Arg Arg Ala Pro Thr Arg Asn Gln Pro Gln Ala Pro Gly
 340 345 350

Val Glu Ala Ser Gly Ala Gly Glu Ala Arg Ala Ser Thr Gly Ser Ser
355 360 365

Asp Ser Ser Pro Gly Gly His Gly Thr Gln Val Asn Val Thr Cys Ile
370 375 380

Val Asn Val Cys Ser Ser Ser Asp His Ser Ser Gln Cys Ser Ser Gln
385 390 395 400

Ala Ser Ser Thr Met Gly Asp Thr Asp Ser Ser Pro Ser Glu Ser Pro
405 410 415

Lys Asp Glu Gln Val Pro Phe Ser Lys Glu Glu Cys Ala Phe Arg Ser
420 425 430

Gln Leu Glu Thr Pro Glu Thr Leu Leu Gly Ser Thr Glu Glu Lys Pro
435 440 445

Leu Pro Leu Gly Val Pro Asp Ala Gly Met Lys Pro Ser
450 455 460

<210> 33
<211> 1475
<212> DNA
<213> Homo sapiens

<400> 33
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agggcccccga cctcgccacc atgagagccc tgctggcgcc cctgcttctc tgcgtcctgg 120
tcgtgagcga ctccaaaggc agcaatgaac ttcattcaagt tccatcgaac tgtgactgtc 180
taaatggagg aacatgtgtg tccaaacaagt acttctccaa cattcactgg tgcaactgcc 240
caagaaatt cggaggggcag cactgtgaaa tagataagtc aaaaacctgc tatgagggga 300
atggtcactt ttaccgagga aaggccagca ctgacaccat gggcgggccc tgccctgccct 360
ggaactctgc cactgtcctt cagcaaactg accatgccca cagatctgat gctcttcagc 420
tggtcctggg gaaacataat tactgcagga acccagacaa ccggaggcga ccctgggtgt 480
atgtgcaggt gggcctaaag ccgcttgtcc aagagtgcgt ggtgcagtgc tgcgcagatg 540
gaaaaaagc ctcctctcct ccagaagaat taaaatttca gtgtggccaa aagactctga 600
ggccccgctt taagattatt gggggagaat tcaccacat cgagaaccag ccctgggttg 660
cgcccatcta caggaggcac cgggggggct ctgtcaccta cgtgtgtgga ggcagcctca 720

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tcagcccttg ctgggtgatac agcgccacac actgcttcat tgattacca aagaaggagg      780
actacatcgt ctacctgggt cgctcaaggc ttaactcaa caccgaagg gagatgaagt      840
ttgaggtgga aaacctatc ctacacaagg actacagcgc tgacaogctt gctcaccaca      900
acgacattgc cttgctgaag atccgttcca aggagggcag gtgtgcgcag ccatcccgga      960
ctatacagac catctgcctg ccctcgatgt ataacgatcc ccagtttggc acaagctgtg     1020
agatcactgg ctttggaata gagaattcta ccgactatct ctatccggag cagctgaaga     1080
tgactgttgt gaagctgatt tcccaccggg agtgtcagca gcccactac tacggctctg     1140
aagtcaccac caaaatgctg tgtgtgctg acccacagtg gaaaacagat tcctgccagg     1200
gagactcagg gggaccctc gtctgttccc tccaaggccg catgactttg actggaattg     1260
tgagctgggg ccgtggatgt gccctgaagg acaagccagg cgtctacacg agagtctcac     1320
acttcttacc ctggatccgc agtcacacca aggaagagaa tggcctggcc ctctgagggg     1380
ccccagggag gaaacgggca ccaccgctt tcttgctggg tgtcattttt gcagtagagt     1440
catctccatc agctgtaaga agagactggg aagat                                  1475

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<210> 34
<211> 431
<212> PRT
<213> Homo sapiens

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<400> 34
```

```

Met Arg Ala Leu Leu Ala Arg Leu Leu Leu Cys Val Leu Val Val Ser
1           5           10           15

```

```

Asp Ser Lys Gly Ser Asn Glu Leu His Gln Val Pro Ser Asn Cys Asp
          20           25           30

```

```

Cys Leu Asn Gly Gly Thr Cys Val Ser Asn Lys Tyr Phe Ser Asn Ile
          35           40           45

```

```

His Trp Cys Asn Cys Pro Lys Lys Phe Gly Gly Gln His Cys Glu Ile
          50           55           60

```

```

Asp Lys Ser Lys Thr Cys Tyr Glu Gly Asn Gly His Phe Tyr Arg Gly
65           70           75           80

```

```

Lys Ala Ser Thr Asp Thr Met Gly Arg Pro Cys Leu Pro Trp Asn Ser
          85           90           95

```


Ala Thr Val Leu Gln Gln Thr Tyr His Ala His Arg Ser Asp Ala Leu
100 105 110

Gln Leu Gly Leu Gly Lys His Asn Tyr Cys Arg Asn Pro Asp Asn Arg
115 120 125

Arg Arg Pro Trp Cys Tyr Val Gln Val Gly Leu Lys Pro Leu Val Gln
130 135 140

Glu Cys Met Val His Asp Cys Ala Asp Gly Lys Lys Pro Ser Ser Pro
145 150 155 160

Pro Glu Glu Leu Lys Phe Gln Cys Gly Gln Lys Thr Leu Arg Pro Arg
165 170 175

Phe Lys Ile Ile Gly Gly Glu Phe Thr Thr Ile Glu Asn Gln Pro Trp
180 185 190

Phe Ala Ala Ile Tyr Arg Arg His Arg Gly Gly Ser Val Thr Tyr Val
195 200 205

Cys Gly Gly Ser Leu Ile Ser Pro Cys Trp Val Ile Ser Ala Thr His
210 215 220

Cys Phe Ile Asp Tyr Pro Lys Lys Glu Asp Tyr Ile Val Tyr Leu Gly
225 230 235 240

Arg Ser Arg Leu Asn Ser Asn Thr Gln Gly Glu Met Lys Phe Glu Val
245 250 255

Glu Asn Leu Ile Leu His Lys Asp Tyr Ser Ala Asp Thr Leu Ala His
260 265 270

His Asn Asp Ile Ala Leu Leu Lys Ile Arg Ser Lys Glu Gly Arg Cys
275 280 285

Ala Gln Pro Ser Arg Thr Ile Gln Thr Ile Cys Leu Pro Ser Met Tyr
290 295 300

Asn Asp Pro Gln Phe Gly Thr Ser Cys Glu Ile Thr Gly Phe Gly Lys
305 310 315 320

Glu Asn Ser Thr Asp Tyr Leu Tyr Pro Glu Gln Leu Lys Met Thr Val
 325 330 335

Val Lys Leu Ile Ser His Arg Glu Cys Gln Gln Pro His Tyr Tyr Gly
 340 345 350

Ser Glu Val Thr Thr Lys Met Leu Cys Ala Ala Asp Pro Gln Trp Lys
 355 360 365

Thr Asp Ser Cys Gln Gly Asp Ser Gly Gly Pro Leu Val Cys Ser Leu
 370 375 380

Gln Gly Arg Met Thr Leu Thr Gly Ile Val Ser Trp Gly Arg Gly Cys
 385 390 395 400

Ala Leu Lys Asp Lys Pro Gly Val Tyr Thr Arg Val Ser His Phe Leu
 405 410 415

Pro Trp Ile Arg Ser His Thr Lys Glu Glu Asn Gly Leu Ala Leu
 420 425 430

<210> 35

<211> 107

<212> PRT

<213> Mus musculus

<400> 35

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
 1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Asp Val Asn Thr Ala
 20 25 30

Val Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
 35 40 45

Tyr Ser Ala Ser Phe Leu Tyr Ser Gly Val Pro Ser Arg Phe Ser Gly
 50 55 60

Ser Arg Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
 65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln His Tyr Thr Thr Pro Pro

85

90

95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
100 105

<210> 36
<211> 120
<212> PRT
<213> Mus musculus

<400> 36

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Asn Ile Lys Asp Thr
20 25 30

Tyr Ile His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ala Arg Ile Tyr Pro Thr Asn Gly Tyr Thr Arg Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Ala Asp Thr Ser Lys Asn Thr Ala Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ser Arg Trp Gly Gly Asp Gly Phe Tyr Ala Met Asp Tyr Trp Gly Gln
100 105 110

Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 37
<211> 120
<212> PRT
<213> Mus musculus

<400> 37

Gln Val Thr Leu Arg Glu Ser Gly Pro Ala Leu Val Lys Pro Thr Gln
1 5 10 15

Thr Leu Thr Thr Cys Thr Phe Ser Gly Phe Ser Leu Ser Thr Ser
 20 25 30

Gly Met Ser Val Gly Trp Ile Arg Gln Pro Ser Gly Lys Ala Leu Glu
 35 40 45

Trp Leu Ala Asp Ile Trp Trp Asp Asp Lys Lys Asp Tyr Asn Pro Ser
 50 55 60

Leu Lys Ser Arg Leu Thr Ile Ser Lys Asp Thr Ser Lys Asn Gln Val
 65 70 75 80

Val Leu Lys Val Thr Asn Met Asp Pro Ala Asp Thr Ala Thr Tyr Tyr
 85 90 95

Cys Ala Arg Ser Met Ile Thr Asn Trp Tyr Phe Asp Val Trp Gly Ala
 100 105 110

Gly Thr Thr Val Thr Val Ser Ser
 115 120

<210> 38
 <211> 106
 <212> PRT
 <213> Mus musculus

<400> 38

Asp Ile Gln Met Thr Gln Ser Pro Ser Thr Leu Ser Ala Ser Val Gly
 1 5 10 15

Asp Arg Val Thr Ile Thr Cys Lys Cys Gln Leu Ser Val Gly Tyr Met
 20 25 30

His Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Trp Ile Tyr
 35 40 45

Asp Thr Ser Lys Leu Ala Ser Gly Val Pro Ser Arg Phe Ser Gly Ser
 50 55 60

Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Asp
 65 70 75 80

Asp Phe Ala Thr Tyr Tyr Cys Phe Gln Gly Ser Gly Tyr Pro Phe Thr
 85 90 95

Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
100 105

<210> 39
<211> 1039
<212> DNA
<213> Homo sapiens

<400> 39
tctgtcacag gcagtgacct gaagtgtctt ttcagagacc tttcttcata gactactttt 60
ttttctttaa gcagcaaaag gagaaaattg tcatcaaagg atattccaga ttcttgacag 120
cattctcgtc atctctgagg acatcaccaat catctcagga tgaggggcat gaagctgctg 180
ggggcgctgc tggcactggc ggcctactcg cagggggcgg tgtccctgaa gatcgcagcc 240
ttcaacatcc agacatttgg ggagaccaag atgtccaatg ccacctcgt cagctacatt 300
gtgcagatcc tgagccgcta tgacatogcc ctgggtccagg aggtcagaga cagccacctg 360
actgcctggt ggaagctgct ggacaacctc aatcaggatg caccagacac ctatcactac 420
gtggtcagtg agccactggg acggaacagc tataaggagc gctacctgtt cgtgtacagg 480
cctgaccagg tgtctgoggt ggacagctac tactacgatg atggctgoga gccctgcggg 540
aacgacacct tcaacogaga gccagccatt gtcaggttct tctccgggtt cacagaggtc 600
agggagtttg ccattgttcc cctgcatgcg gcccggggg acgcagtagc cgagatcgac 660
gctctctatg acgtctacct ggatgtccaa gagaatggg gcttgaggga cgtcatgttg 720
atgggcgact tcaatgcggg ctgcagctat gtgagacctt ccagtggtc atccatccgc 780
ctgtggacaa gcccacett ccagtggtg atccccgaca gcgtgacac cacagctaca 840
cccacgcact gtgcctatga caggatcggt gttgcaggga tgcgtctcg aggcgcggtt 900
gttcccgact oggctcttcc cttaacttc caggctgcct atggcctgag tgaccaactg 960
gcccagcca tcagtgacca ctatccagtg gaggtgatgc tgaagtgage agccctccc 1020
cacaccagtt gaactgcag 1039

<210> 40
<211> 282
<212> PRT
<213> Homo sapiens

<400> 40

Met Arg Gly Met Lys Leu Leu Gly Ala Leu Leu Ala Leu Ala Ala Leu

1	5	10	15
Leu Gln Gly Ala Val Ser Leu Lys Ile Ala Ala Phe Asn Ile Gln Thr	20	25	30
Phe Gly Glu Thr Lys Met Ser Asn Ala Thr Leu Val Ser Tyr Ile Val	35	40	45
Gln Ile Leu Ser Arg Tyr Asp Ile Ala Leu Val Gln Glu Val Arg Asp	50	55	60
Ser His Leu Thr Ala Val Gly Lys Leu Leu Asp Asn Leu Asn Gln Asp	65	70	75
Ala Pro Asp Thr Tyr His Tyr Val Val Ser Glu Pro Leu Gly Arg Asn	85	90	95
Ser Tyr Lys Glu Arg Tyr Leu Phe Val Tyr Arg Pro Asp Gln Val Ser	100	105	110
Ala Val Asp Ser Tyr Tyr Tyr Asp Asp Gly Cys Glu Pro Cys Gly Asn	115	120	125
Asp Thr Phe Asn Arg Glu Pro Ala Ile Val Arg Phe Phe Ser Arg Phe	130	135	140
Thr Glu Val Arg Glu Phe Ala Ile Val Pro Leu His Ala Ala Pro Gly	145	150	155
Asp Ala Val Ala Glu Ile Asp Ala Leu Tyr Asp Val Tyr Leu Asp Val	165	170	175
Gln Glu Lys Trp Gly Leu Glu Asp Val Met Leu Met Gly Asp Phe Asn	180	185	190
Ala Gly Cys Ser Tyr Val Arg Pro Ser Gln Trp Ser Ser Ile Arg Leu	195	200	205
Trp Thr Ser Pro Thr Phe Gln Trp Leu Ile Pro Asp Ser Ala Asp Thr	210	215	220
Thr Ala Thr Pro Thr His Cys Ala Tyr Asp Arg Ile Val Val Ala Gly	225	230	235
			240

Met Leu Leu Arg Gly Ala Val Val Pro Asp Ser Ala Leu Pro Phe Asn
 245 250 255

Phe Gln Ala Ala Tyr Gly Leu Ser Asp Gln Leu Ala Gln Ala Ile Ser
 260 265 270

Asp His Tyr Pro Val Glu Val Met Leu Lys
 275 280

<210> 41
 <211> 678
 <212> DNA
 <213> Mus musculus

<400> 41
 gacatcttgc tgactcagtc tccagccatc ctgtctgtga gtccaggaga aagagtcagt 60
 ttctcctgca gggccagtc gttcgttggc tcaagcatcc actggtatca gcaaagaaca 120
 aatggttctc caaggtctct cataaagtat gcttctgagt ctatgtctgg gatcccttc 180
 aggttttagtg gcagtggtac agggacagat ttactctta gcatcaacac tgtggagtct 240
 gaagatatgg cagattatta ctgtcaacaa agtcatagct ggccattcac gttcggctcg 300
 gggacaaatt tggaagtaaa agaagtgaag cttgaggagt ctggaggagg cttggtgcaa 360
 cctggaggat ccatgaaact ctctgtgtt gcctctggat tcattttcag taaccactgg 420
 atgaactggg tccgccagtc tccagagaag ggccttgagt gggttgctga aattagatca 480
 aaatctatta attctgcaac acattatgag gactctgtga aaggagggtt caccatctca 540
 agagatgatt ccaaaagtc tgtctacctg caaatgaccg acttaagaac tgaagacact 600
 ggcgtttatt actgttccag gaattactac ggtagtacct acgactactg gggccaaggg 660
 accactctca cagtctcc 678

<210> 42
 <211> 226
 <212> PRT
 <213> Mus musculus

<400> 42

Asp Ile Leu Leu Thr Gln Ser Pro Ala Ile Leu Ser Val Ser Pro Gly
 1 5 10 15

Glu Arg Val Ser Phe Ser Cys Arg Ala Ser Gln Phe Val Gly Ser Ser

20	25	30
Ile His Trp Tyr Gln Gln Arg Thr Asn Gly Ser Pro Arg Leu Leu Ile 35 40 45		
Lys Tyr Ala Ser Glu Ser Met Ser Gly Ile Pro Ser Arg Phe Ser Gly 50 55 60		
Ser Gly Ser Gly Thr Asp Phe Thr Leu Ser Ile Asn Thr Val Glu Ser 65 70 75 80		
Glu Asp Ile Ala Asp Tyr Tyr Cys Gln Gln Ser His Ser Trp Pro Phe 85 90 95		
Thr Phe Gly Ser Gly Thr Asn Leu Glu Val Lys Glu Val Lys Leu Glu 100 105 110		
Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Met Lys Leu Ser 115 120 125		
Cys Val Ala Ser Gly Phe Ile Phe Ser Asn His Trp Met Asn Trp Val 130 135 140		
Arg Gln Ser Pro Glu Lys Gly Leu Glu Trp Val Ala Glu Ile Arg Ser 145 150 155 160		
Lys Ser Ile Asn Ser Ala Thr His Tyr Ala Glu Ser Val Lys Gly Arg 165 170 175		
Phe Thr Ile Ser Arg Asp Asp Ser Lys Ser Ala Val Tyr Leu Gln Met 180 185 190		
Thr Asp Leu Arg Thr Glu Asp Thr Gly Val Tyr Tyr Cys Ser Arg Asn 195 200 205		
Tyr Tyr Gly Ser Thr Tyr Asp Tyr Trp Gly Gln Gly Thr Thr Leu Thr 210 215 220		
Val Ser 225		
<210> 43		
<211> 450		

<212> DNA

<213> Homo sapiens

```

<400> 43
gctgcatcag aagaggccat caagcacatc actgtccttc tgccatggcc ctgtggatgc      60
gectcctgcc cctgctggcg ctgctggccc tctggggacc tgaccagcc gcagcctttg      120
tgaaccaaca cctgtggggc tcacacctgg tggaaagtct ctacctagtg tgcgggggaa      180
gaggtcttct ctacacaccc aagaccggcc gggaggcaga ggacctgcag gtgggggcagg      240
tggagctggg cggggggccct ggtgcaggca gctgcagcc cttggccctg gagggggtccc      300
tgcagaagcg tggcattgtg gaacaatgct gtaccagcat ctgctccctc taccagctgg      360
agaactactg caactagacg cagcccgag gcagccccc acccgccgcc tctgcaccg      420
agagagatgg aataaagccc ttgaaccagg      450

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<210> 44

<211> 110

<212> PRT

<213> Homo sapiens

<400> 44

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Met Ala Leu Trp Met Arg Leu Leu Pro Leu Leu Ala Leu Leu Ala Leu
1           5           10          15

```

```

Trp Gly Pro Asp Pro Ala Ala Ala Phe Val Asn Gln His Leu Cys Gly
20          25          30

```

```

Ser His Leu Val Glu Ala Leu Tyr Leu Val Cys Gly Glu Arg Gly Phe
35          40          45

```

```

Phe Tyr Thr Pro Lys Thr Arg Arg Glu Ala Glu Asp Leu Gln Val Gly
50          55          60

```

```

Gln Val Glu Leu Gly Gly Gly Pro Gly Ala Gly Ser Leu Gln Pro Leu
65          70          75          80

```

```

Ala Leu Glu Gly Ser Leu Gln Lys Arg Gly Ile Val Glu Gln Cys Cys
85          90          95

```

```

Thr Ser Ile Cys Ser Leu Tyr Gln Leu Glu Asn Tyr Cys Asn
100         105         110

```

<210> 45

<211> 1203
 <212> DNA
 <213> Hepatitis B virus

<400> 45
 atgggaggtt ggtcttccaa acctcgacaa ggcattggga cgaatcttcc tgttcccaat 60
 cctctgggat tctttccgga tcaccagttg gacctgcgtg tcggagccaa ctcaacaat 120
 ccagattggg aottcaacc caacaaggat cactggccag aggcaatcaa ggtaggagcg 180
 ggagacttcg ggcaggggtt cccccacca caccggcggtc ttttggggtg gagccctcag 240
 gctcagggca tattgacaac agtgccagca gcgcctcctc ctgtttccac caatcggcag 300
 tcaggaagac agcctactcc catctctcca cctctaagag acagtcaccc tcaggccatg 360
 cagtggaaact ccacaacatt ccaccaagct ctgctagatc ccagagtggg gggcctatat 420
 tttctctctg gtggctccag ttccgggaaca gtaaaccttg ttccgactac tgtctcacc 480
 atatcgtaaa tcttctcgag gactggggac cctgcaccga acatggagag cacaacatca 540
 ggattcttag gacctctgct cgtgttacag gcgggggttt tcttgttgac aagaatcctc 600
 acaataccac agagtctaga ctctgtgttg acttctctca atttcttagg gggagcacc 660
 acgtgtcctg gccaaaattc gcagtcacca acctccaac actcaccaac ctcttgcct 720
 ccaatttgct ctggttatcg ctggatgtgt ctgcgggctt ttatcatatt cctcttcac 780
 ctgctgctat gctcatctt cttgttggtt cttctggact accaaggatg gttgcccgtt 840
 tgtctctac ttccaggaac atcaactacc agcacgggac catgcaagac ctgcacgatt 900
 cctgctcaag gaacctctat gtttccctct tgttctgta caaaaccttc ggacggaaac 960
 tgcaattgta ttcccatccc atcatcctgg gctttcgcaa gattcctatg ggagtgggcc 1020
 tcagtcggtt tctcctggct cagtttacta gtgccatttg ttcagtgggt cgcagggtt 1080
 tcccactg tttggcttcc agttatatgg atgatgtggt attgggggcc aagtctgtac 1140
 aacatcttga gtcccttttt acctctatta ccaattttct tttgtctttg ggtatacat 1200
 tga 1203

<210> 46
 <211> 400
 <212> PRT
 <213> Hepatitis B virus

<400> 46

Met Gly Gly Trp Ser Ser Lys Pro Arg Gln Gly Met Gly Thr Asn Leu
 1 5 10 15

Ser Val Pro Asn Pro Leu Gly Phe Phe Pro Asp His Gln Leu Asp Pro
 20 25 30

Ala Phe Gly Ala Asn Ser Asn Asn Pro Asp Trp Asp Phe Asn Pro Asn
 35 40 45

Lys Asp His Trp Pro Glu Ala Ile Lys Val Gly Ala Gly Asp Phe Gly
 50 55 60

Pro Gly Phe Thr Pro Pro His Gly Gly Leu Leu Gly Trp Ser Pro Gln
 65 70 75 80

Ala Gln Gly Ile Leu Thr Thr Val Pro Ala Ala Pro Pro Pro Val Ser
 85 90 95

Thr Asn Arg Gln Ser Gly Arg Gln Pro Thr Pro Ile Ser Pro Pro Leu
 100 105 110

Arg Asp Ser His Pro Gln Ala Met Gln Trp Asn Ser Thr Thr Phe His
 115 120 125

Gln Ala Leu Leu Asp Pro Arg Val Arg Gly Leu Tyr Phe Pro Ala Gly
 130 135 140

Gly Ser Ser Ser Gly Thr Val Asn Pro Val Pro Thr Thr Val Ser Pro
 145 150 155 160

Ile Ser Ser Ile Phe Ser Arg Thr Gly Asp Pro Ala Pro Asn Met Glu
 165 170 175

Ser Thr Thr Ser Gly Phe Leu Gly Pro Leu Leu Val Leu Gln Ala Gly
 180 185 190

Phe Phe Leu Leu Thr Arg Ile Leu Thr Ile Pro Gln Ser Leu Asp Ser
 195 200 205

Trp Trp Thr Ser Leu Asn Phe Leu Gly Gly Ala Pro Thr Cys Pro Gly
 210 215 220

Gln Asn Ser Gln Ser Pro Thr Ser Asn His Ser Pro Thr Ser Cys Pro
 225 230 235 240

Pro Ile Cys Pro Gly Tyr Arg Trp Met Cys Leu Arg Arg Phe Ile Ile
245 250 255

Phe Leu Phe Ile Leu Leu Leu Cys Leu Ile Phe Leu Leu Val Leu Leu
260 265 270

Asp Tyr Gln Gly Met Leu Pro Val Cys Pro Leu Leu Pro Gly Thr Ser
275 280 285

Thr Thr Ser Thr Gly Pro Cys Lys Thr Cys Thr Ile Pro Ala Gln Gly
290 295 300

Thr Ser Met Phe Pro Ser Cys Cys Cys Thr Lys Pro Ser Asp Gly Asn
305 310 315 320

Cys Thr Cys Ile Pro Ile Pro Ser Ser Trp Ala Phe Ala Arg Phe Leu
325 330 335

Trp Glu Trp Ala Ser Val Arg Phe Ser Trp Leu Ser Leu Leu Val Pro
340 345 350

Phe Val Gln Trp Phe Ala Gly Leu Ser Pro Thr Val Trp Leu Ser Val
355 360 365

Ile Trp Met Met Trp Tyr Trp Gly Pro Ser Leu Tyr Asn Ile Leu Ser
370 375 380

Pro Phe Leu Pro Leu Leu Pro Ile Phe Phe Cys Leu Trp Val Tyr Ile
385 390 395 400

<210> 47

<211> 799

<212> DNA

<213> Homo sapiens

<400> 47

cgaccactc agggctctgt ggacagctca cctagctgca atggctacag gctcccgga	60
gtccctgtct ctgggttttg gctgctctg cctgccttg cttcaagagg gcagtgcctt	120
cccaaccatt cccttatcca gcccttttga caacgctatg ctccggcccc atcgtctgca	180
ccagctggcc tttagacacct accaggagtt tgaagaagcc tatatcccaa aggaacagaa	240
gtattcatte ctgcagaacc ccagacctc cctctgttcc tcagagtcta ttccgacacc	300

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ctccaacagg gaggaaacac aacagaaatc caacctagag ctgctccgca tctccctgct 360
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<210> 48
<211> 217
<212> PRT
<213> Homo sapiens

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<400> 48
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Met Ala Thr Gly Ser Arg Thr Ser Leu Leu Leu Ala Phe Gly Leu Leu
1           5           10          15

```

```

Cys Leu Pro Trp Leu Gln Glu Gly Ser Ala Phe Pro Thr Ile Pro Leu
          20          25          30

```

```

Ser Arg Pro Phe Asp Asn Ala Met Leu Arg Ala His Arg Leu His Gln
          35          40          45

```

```

Leu Ala Phe Asp Thr Tyr Gln Glu Phe Glu Glu Ala Tyr Ile Pro Lys
          50          55          60

```

```

Glu Gln Lys Tyr Ser Phe Leu Gln Asn Pro Gln Thr Ser Leu Cys Phe
65          70          75          80

```

```

Ser Glu Ser Ile Pro Thr Pro Ser Asn Arg Glu Glu Thr Gln Gln Lys
          85          90          95

```

```

Ser Asn Leu Glu Leu Leu Arg Ile Ser Leu Leu Leu Ile Gln Ser Trp
          100          105          110

```

```

Leu Glu Pro Val Gln Phe Leu Arg Ser Val Phe Ala Asn Ser Leu Val
          115          120          125

```

Tyr Gly Ala Ser Asp Ser Asn Val Tyr Asp Leu Leu Lys Asp Leu Glu
 130 135 140

Glu Gly Ile Gln Thr Leu Met Gly Arg Leu Glu Asp Gly Ser Pro Arg
 145 150 155 160

Thr Gly Gln Ile Phe Lys Gln Thr Tyr Ser Lys Phe Asp Thr Asn Ser
 165 170 175

His Asn Asp Asp Ala Leu Leu Lys Asn Tyr Gly Leu Leu Tyr Cys Phe
 180 185 190

Arg Lys Asp Met Asp Lys Val Glu Thr Phe Leu Arg Ile Val Gln Cys
 195 200 205

Arg Ser Val Glu Gly Ser Cys Gly Phe
 210 215

<210> 49
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 <212> DNA
 <213> Homo sapiens

<400> 49
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<210> 50
<211> 320
<212> PRT
<213> Homo sapiens

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<400> 50

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Met Glu Thr Asp Thr Leu Leu Leu Trp Val Leu Leu Leu Trp Val Pro
1          5          10          15

```

```

Gly Ser Thr Gly Asp Val Arg Arg Gly Pro Arg Ser Leu Arg Gly Arg
          20          25          30

```

```

Asp Ala Pro Ala Pro Thr Pro Cys Val Pro Ala Glu Cys Phe Asp Leu
          35          40          45

```

```

Leu Val Arg His Cys Val Ala Cys Gly Leu Leu Arg Thr Pro Arg Pro
          50          55          60

```

```

Lys Pro Ala Gly Ala Ser Ser Pro Ala Pro Arg Thr Ala Leu Gln Pro
65          70          75          80

```

```

Gln Glu Ser Val Gly Ala Gly Ala Gly Glu Ala Ala Val Asp Lys Thr
          85          90          95

```

```

His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser
          100          105          110

```

```

Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg
          115          120          125

```

```

Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro
          130          135          140

```

```

Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala
          145          150          155          160

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Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val

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165

170

175

Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr
 180 185 190

Lys Cys Lys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr
 195 200 205

Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu
 210 215 220

Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys
 225 230 235 240

Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser
 245 250 255

Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp
 260 265 270

Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser
 275 280 285

Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala
 290 295 300

Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
 305 310 315 320

<210> 51

<211> 107

<212> PRT

<213> Homo sapiens

<400> 51

Asp Ile Gln Met Thr Gln Thr Pro Ser Thr Leu Ser Ala Ser Val Gly
 1 5 10 15

Asp Arg Val Thr Ile Ser Cys Arg Ala Ser Gln Asp Ile Asn Asn Tyr
 20 25 30

Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
 35 40 45

Tyr Tyr Thr Ser Thr Leu His Ser Gly Val Pro Ser Arg Phe Ser Gly
 50 55 60

Ser Gly Ser Gly Thr Asp Tyr Thr Leu Thr Ile Ser Ser Leu Gln Pro
 65 70 75 80

Asp Asp Phe Ala Thr Tyr Phe Cys Gln Gln Gly Asn Thr Leu Pro Trp
 85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Val Lys
 100 105

<210> 52

<211> 107

<212> PRT

<213> Mus musculus

<400> 52

Asp Ile Gln Met Thr Gln Thr Thr Ser Ser Leu Ser Ala Ser Leu Gly
 1 5 10 15

Asp Arg Val Thr Ile Ser Cys Arg Ala Ser Gln Asp Ile Asn Asn Tyr
 20 25 30

Leu Asn Trp Tyr Gln Gln Lys Pro Asp Gly Ile Val Lys Leu Leu Ile
 35 40 45

Tyr Tyr Thr Ser Thr Leu His Ser Gly Val Pro Ser Arg Phe Ser Gly
 50 55 60

Ser Gly Ser Gly Thr Asp Tyr Ser Leu Thr Ile Ser Asn Leu Glu Gln
 65 70 75 80

Glu Asp Ile Ala Thr Tyr Phe Cys Gln Gln Gly Asn Thr Leu Pro Trp
 85 90 95

Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
 100 105

<210> 53

<211> 119

<212> PRT

<213> Homo sapiens

<400> 53

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser
 1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Ala Phe Thr Asn Tyr
 20 25 30

Leu Ile Glu Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile
 35 40 45

Gly Val Ile Tyr Pro Gly Ser Gly Gly Thr Asn Tyr Asn Glu Lys Phe
 50 55 60

Lys Gly Arg Val Thr Leu Thr Val Asp Glu Ser Thr Asn Thr Ala Tyr
 65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Phe Cys
 85 90 95

Ala Arg Arg Asp Gly Asn Tyr Gly Trp Phe Ala Tyr Trp Gly Gln Gly
 100 105 110

Thr Leu Val Thr Val Ser Ser
 115

<210> 54

<211> 119

<212> PRT

<213> Mus musculus

<400> 54

Gln Val Gln Leu Gln Gln Ser Gly Ala Glu Leu Val Gly Pro Gly Thr
 1 5 10 15

Ser Val Arg Val Ser Cys Lys Ala Ser Gly Tyr Ala Phe Thr Asn Tyr
 20 25 30

Leu Ile Glu Trp Val Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile
 35 40 45

Gly Val Ile Tyr Pro Gly Ser Gly Gly Thr Asn Tyr Asn Glu Lys Phe
 50 55 60

Lys Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Thr Thr Ala Tyr
65 70 75 80

Met Gln Leu Ser Ser Leu Thr Ser Asp Asp Ser Ala Val Tyr Phe Cys
85 90 95

Ala Arg Arg Asp Gly Asn Tyr Gly Trp Phe Ala Tyr Trp Gly Arg Gly
100 105 110

Thr Leu Val Thr Val Ser Ala
115

<210> 55
<211> 214
<212> PRT
<213> Homo sapiens

<400> 55

Asp Ile Gln Met Thr Gln Thr Pro Ser Thr Leu Ser Ala Ser Val Gly
1 5 10 15

Asp Arg Val Thr Ile Ser Cys Arg Ala Ser Gln Asp Ile Asn Asn Tyr
20 25 30

Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
35 40 45

Tyr Tyr Thr Ser Thr Leu His Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Asp Tyr Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

Asp Asp Phe Ala Thr Tyr Phe Cys Gln Gln Gly Asn Thr Leu Pro Trp
85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Val Lys Arg Thr Val Ala Ala
100 105 110

Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly
115 120 125

Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala
130 135 140

Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln
 145 150 155 160

Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser
 165 170 175

Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr
 180 185 190

Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser
 195 200 205

Phe Asn Arg Gly Glu Cys
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<210> 56
 <211> 448
 <212> PRT
 <213> Homo sapiens

<400> 56

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser
 1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Ala Phe Thr Asn Tyr
 20 25 30

Leu Ile Glu Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile
 35 40 45

Gly Val Ile Tyr Pro Gly Ser Gly Gly Thr Asn Tyr Asn Glu Lys Phe
 50 55 60

Lys Gly Arg Val Thr Leu Thr Val Asp Glu Ser Thr Asn Thr Ala Tyr
 65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Phe Cys
 85 90 95

Ala Arg Arg Asp Gly Asn Tyr Gly Trp Phe Ala Tyr Trp Gly Gln Gly
 100 105 110

Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe
 115 120 125

Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu
 130 135 140

Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp
 145 150 155 160

Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu
 165 170 175

Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser
 180 185 190

Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro
 195 200 205

Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys
 210 215 220

Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro
 225 230 235 240

Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser
 245 250 255

Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp
 260 265 270

Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn
 275 280 285

Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val
 290 295 300

Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu
 305 310 315 320

Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys
 325 330 335

Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr

340

345

350

Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr
 355 360 365

Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu
 370 375 380

Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu
 385 390 395 400

Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys
 405 410 415

Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu
 420 425 430

Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly
 435 440 445

<210> 57

<211> 8540

<212> DNA

<213> Homo sapiens

<400> 57

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